

(19) World Intellectual Property  
Organization  
International Bureau



(43) International Publication Date  
1 April 2004 (01.04.2004)

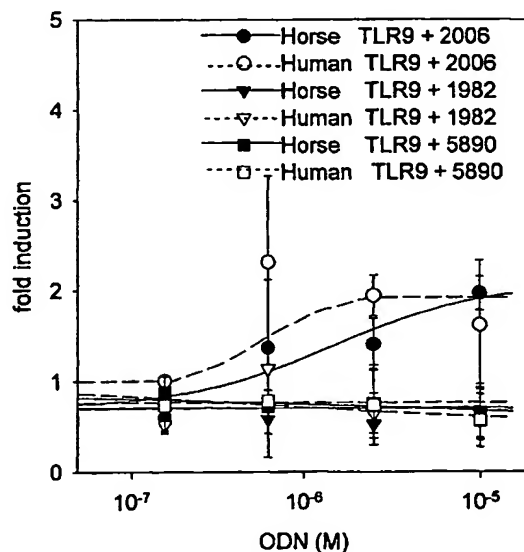
PCT

(10) International Publication Number  
**WO 2004/026888 A2**

- (51) International Patent Classification<sup>7</sup>: **C07H**
- (21) International Application Number:  
PCT/US2003/029577
- (22) International Filing Date:  
19 September 2003 (19.09.2003)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:  
60/412,479 19 September 2002 (19.09.2002) US
- (72) Inventors; and  
(75) Inventors/Applicants (for US only): **LIPFORD, Grayson, B.** [US/US]; 38 Bates Road, Watertown, MA 02472 (US). **MOOKHERJEE, Neeloffer** [IN/CA]; Apt 408, 2233 Allison Road,, Vancouver, BC V6T 1T7 (CA). **BABIUK, Lorne** [CA/CA]; 245 East Place, Saskatoon, Saskatchewan S7J 2Y1 (CA). **BROWNLIE, Robert** [CA/CA]; 123 O'Brien Crescent, Saskatoon, Saskatchewan S7K 5K3 (CA). **GRIEBEL, Phillip** [CA/CA]; Box 36, RR5, Saskatoon, Saskatchewan S7K 3J8 (CA). **MUTWIRI, George** [CA/CA]; 569 Nordstrum Road, Saskatoon, Saskatchewan S7K 7X6 (CA). **HECKER, Rolf** [DE/DE]; Benrodestr. 60, 40597 Düsseldorf (DE).
- (74) Agent: **STEELE, Alan, W.**; Wolf, Greenfield & Sacks, P.C., 600 Atlantic Avenue, Boston, MA 02210 (US).
- (81) Designated States (national): AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX,

[Continued on next page]

(54) Title: TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES



(57) Abstract: Novel amino acid and nucleotide sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) Toll-like receptor 9 (TLR9) are provided. Also provided are amino acid and nucleotide sequences for dog (canine), cat (feline), mouse (murine), and human TLR9. Comparison of these sequences, especially in combination with functional assessment for species-specific CpG motif preferences, permits identification of specific regions and amino acid residues of interest in TLR9 ligand interaction. Novel chimeric TLR9 receptor molecules, cells expressing these molecules, and methods for their use in screening assays for TLR9 ligands are also provided.

WO 2004/026888 A2



MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

**Published:**

— without international search report and to be republished upon receipt of that report

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO,

*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

## TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES

### Background of the Invention

Synthetic oligodeoxynucleotides (ODN) and DNA containing immunostimulatory CpG motifs (CpG DNA) function as potent adjuvants and activators of the innate immune system. Heeg K et al. (2000) *Int Arch Allergy Immunol* 121:87-97; Krieg AM (2001) *Vaccine* 19:618-22. A wide variety of CpG-containing sequences have been screened for biological activity and it is reported that optimal CpG DNA sequences can vary among species. Rankin R et al. (2001) *Antisense Nucleic Acid Drug Dev* 11:333-40.

Toll-like receptor 9 (TLR9) has recently been identified as a receptor for CpG ODN. Hemmi H et al. (2000) *Nature* 408:740-5. The molecular mechanism by which TLR9 recognizes CpG DNA is not understood.

### Summary of the Invention

Toll-like receptor 9 (TLR9) is known to be involved in innate immunity and to signal in response to CpG DNA. To date, the amino acid sequences only of human and murine TLR9 have been reported, and, interestingly, these two species are known to prefer different CpG motifs. The structural basis for this species-specific CpG motif preference has not yet been fully elucidated. The instant invention provides, in part, novel amino acid and nucleotide sequences of rat, pig, cow, and horse TLR9. These novel TLR9 sequences are useful for elucidating certain key structural features of TLR9. Specifically, comparison of sequences of murine, human, and these novel TLR9 sequences permits identification of areas of highly conserved sequence, areas of group conservation, and areas of hypervariability. In addition, such comparisons permit an assessment of evolutionary relatedness among TLR9 molecules of the various species, as well as an assessment of inter-species homologies. Importantly, such comparisons permit a rational basis for identifying amino acids in TLR9 that may be involved in the CpG binding site, as well as amino acids involved in conferring species specificity for particular CpG motifs. Such information may be used to design and construct novel TLR9 molecules which incorporate specific point or regional mutations and which possess desired ligand binding characteristics. Such information may also be useful in designing and identifying novel ligands for TLR9 of a given species.

- 2 -

In one aspect, the invention provides isolated polypeptides having amino acid sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) TLR9 polypeptides. These amino acid sequences correspond to SEQ ID NOs 1, 5, 9, 13, and 17, respectively. Each of these sequences is believed to include at least a majority of an extracellular domain, as well as a transmembrane region and at least part of a TLR/IL-1 receptor (TIR) domain. To the extent any such sequence may lack an amino-terminal and/or carboxy-terminal sequence, such sequence is ascertainable, without undue experimentation, using conventional molecular biology techniques and the sequence information provided herein.

In another aspect the invention provides isolated polypeptides having amino acid sequences for essentially the whole extracellular domain, optionally including a signal peptide, of each of rat, porcine, bovine, equine, and ovine TLR9. These amino acid sequences correspond to SEQ ID NOs 2, 6, 10, 14, and 18, respectively. Such extracellular domains are believed to include sequence specifically involved in binding to TLR9 ligand, such as CpG DNA. In addition, such extracellular domains are believed to include sequence that confers species specificity for particular CpG motifs.

Isolated nucleic acid molecules encoding the polypeptides just described above are also provided according to further aspects of the invention. Such nucleic acid molecules include, but are not limited to, nucleic acid molecules having sequences provided by SEQ ID NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively. Isolated nucleic acid molecules encoding the TLR9 polypeptides of SEQ ID NOs 1, 5, 9, 13, 17; and 2, 6, 10, 14, and 18 also include nucleic acid molecules that differ in sequence from SEQ ID NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively, due to degeneracy of the genetic code. Such nucleic acid molecules will hybridize, under stringent conditions, with suitably selected nucleic acid molecules having sequences selected from SEQ ID NOs 3, 4, 7, 8, 11, 12, 15, 16, 19, and 20.

In another aspect the invention provides a vector which includes an isolated nucleic acid molecule of the invention. In one embodiment the vector is an expression vector and the isolated nucleic acid molecule of the invention is operably linked to a regulatory sequence in the vector. When present within a cell, an expression vector according to this aspect of the invention causes the cell to express a polypeptide of the invention.

The invention according to another aspect provides a cell in which a vector of the invention is present. In one embodiment the cell containing the vector expresses a



- 3 -

polypeptide of the invention. In certain embodiments the cell also contains a reporter construct that transduces a TLR9-mediated signal in response to contact of the polypeptide of the invention or a TLR9 with a suitable TLR9 ligand. The cell containing the vector, and optionally containing the reporter construct, can be used in screening methods also provided  
5 by the invention.

In yet another aspect the invention provides an antibody or antibody fragment that binds specifically to an isolated polypeptide of the invention. In certain embodiments the antibody or antibody fragment binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide. More specifically, the antibody or antibody fragment binds uniquely to  
10 one of the isolated polypeptides of the invention. In one embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide also binds to either mouse or human TLR9. In another embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide does not also bind to either mouse or human TLR9. In some embodiments  
15 the antibody or antibody fragment binds selectively to a chimeric TLR9 polypeptide of the invention. In certain embodiments the antibody or antibody fragment of the invention is a monoclonal antibody or fragment of a monoclonal antibody.

In one aspect the invention provides a method for identifying key amino acids in a TLR9 of a first species which confer specificity for CpG DNA optimized for TLR9 of the  
20 first species. The method involves aligning protein sequences of TLR9 of a first species, TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species; generating an initial set of candidate amino acids in the TLR9 of the  
25 first species by excluding each amino acid in the TLR9 of the first species which (a) is identical with the TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with the TLR9 of the third species or (b)  
30 differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

- 4 -

In another aspect the invention provides a method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9. The method according to this aspect of the invention involves aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a CpG DNA optimized for murine TLR9; generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids. In one embodiment the method according to this aspect of the invention is performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred CpG DNA).

In another aspect the invention also provides an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:30 (extracellular domain (ECD) of murine TLR9) except for substitution of at least one key amino acid identified according to the method above. The polypeptide according to this aspect of the invention is a chimeric TLR9 polypeptide. Preferably the polypeptide according to this aspect of the invention binds to CpG DNA optimized for human TLR9 better than does the isolated polypeptide having an amino acid sequence identical to SEQ ID NO:30 (ECD of murine TLR9). In one embodiment the polypeptide includes only one substituted amino acid. The isolated polypeptide according to this aspect of the invention may further include sequence involved in TLR/IL-1R signal transduction, e.g., intracellular domain of TLR9 as provided in SEQ ID NOs 29 and 33. For example, in one embodiment a polypeptide according to this aspect of the invention is an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:29 (full length murine TLR9) except for substitution of at least one key amino acid identified according to the method above.

- 5 -

In another aspect the invention provides an isolated nucleic acid molecule including a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described. In one embodiment the isolated nucleic acid molecule has a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described.

5 In yet another aspect, the invention provides a screening method to identify a TLR9 ligand. The method involves contacting a polypeptide (including a chimeric TLR9 polypeptide) of the invention with a candidate TLR9 ligand; measuring a signal in response to the contacting; and identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling. In one embodiment  
10 the candidate TLR9 ligand is an immunostimulatory nucleic acid. In one embodiment the candidate TLR9 ligand is a CpG DNA.

The invention also provides, in yet a further aspect, a screening method to identify species-specific CpG-motif preference of an isolated polypeptide of the invention. The method according to this aspect of the invention involves contacting an isolated polypeptide  
15 of the invention with a CpG DNA including a hexamer sequence selected from the group consisting of GACGTT, AACGTT, CACGTT, TACGTT, GGCGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG; measuring a signal in response to the contacting; and identifying a species-specific CpG-motif preference when the signal in  
20 response to the contacting is consistent with TLR9 signaling. In one embodiment the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

	TCCATGACGTTTTTGATGTT	(SEQ ID NO:39),
	TCCATAACGTTTTTGATGTT	(SEQ ID NO:40),
	TCCATCACGTTTTTGATGTT	(SEQ ID NO:41),
25	TCCATTACGTTTTTGATGTT	(SEQ ID NO:42),
	TCCATGGCGTTTTTGATGTT	(SEQ ID NO:43),
	TCCATGCCGTTTTTGATGTT	(SEQ ID NO:44),
	TCCATGTCGTTTTTGATGTT	(SEQ ID NO:45),
	TCCATGATGTTTTTGATGTT	(SEQ ID NO:46),
30	TCCATGAAGTTTTTGATGTT	(SEQ ID NO:47),
	TCCATGAGGTTTTTGATGTT	(SEQ ID NO:48),
	TCCATGACATTTTTGATGTT	(SEQ ID NO:49),
	TCCATGACCTTTTTGATGTT	(SEQ ID NO:50),
	TCCATGACTTTTTTGATGTT	(SEQ ID NO:51),
35	TCCATGACGCTTTTTGATGTT	(SEQ ID NO:52),
	TCCATGACGATTTTTGATGTT	(SEQ ID NO:53),
	TCCATGACGGTTTTGATGTT	(SEQ ID NO:54),

- 6 -

TCCATGACGTCTTTGATGTT (SEQ ID NO:55),  
 TCCATGACGTATTTGATGTT (SEQ ID NO:56), and  
 TCCATGACGTGTTTGATGTT (SEQ ID NO:57).

In certain embodiments of the screening methods of the invention, the signal includes  
 5 expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway. In one  
 embodiment the reporter gene is operatively linked to a promoter sensitive to NF- $\kappa$ B. In one  
 embodiment the signal in response to contacting is binding of the candidate TLR9 ligand or  
 CpG DNA to the polypeptide of the invention.

In one embodiment the screening method is performed on a plurality of test  
 10 compounds. In one embodiment the response mediated by the TLR9 signal transduction  
 pathway is measured quantitatively and the response mediated by the TLR9 signal  
 transduction pathway associated with each of the plurality of test compounds is compared  
 with a response arising as a result of an interaction between the functional TLR9 and a  
 reference immunostimulatory compound.

15

#### Brief Description of the Figures

Figure 1 depicts a Clustal W multiple sequence alignment of deduced amino acid  
 sequences for cat (feline), dog (canine), cow (bovine), mouse (murine), sheep (ovine), pig  
 (porcine), horse (equine), human, and rat TLR9 polypeptides. The deduced amino acid  
 20 sequences for feline, canine, bovine, murine, ovine, porcine, equine, human, and rat TLR9  
 polypeptides shown in the figure correspond to SEQ ID NOs 25, 21, 9, 29, 17, 5, 13, 33, and  
 1, respectively. Lines labeled "multiple" refer to the multiple sequence alignment of all six  
 sequences shown. Lines labeled "mo/hu" refer to a paired sequence alignment of mouse and  
 human TLR9 sequences alone.

25 Figure 2 is a cladogram depicting an evolutionary relatedness tree for rat, murine,  
 porcine, bovine, equine, and human TLR9 polypeptides in Figure 1.

Figure 3 is a graph depicting species specificity of TLR9 signaling with selected  
 oligonucleotides having strong specificity for human (2006), mouse (5890), or neither (1982).

30

#### Detailed Description of the Invention

The present invention provides novel amino acid and nucleotide sequences for TLR9  
 derived from rat, pig, cow, horse, and sheep. These sequences can be used to identify key  
 features of the primary sequences of these and related TLR molecules, including previously

- 7 -

known primary sequences of human and mouse (murine) TLR9. Such key features include binding site information and species specificity toward particular CpG motifs. Native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed in vitro or in vivo and used in screening assays to identify and to design novel TLR9 ligands.

5 Additionally, the native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed in vitro or in vivo and used in screening assays to compare various TLR9 ligands, including CpG DNA.

In one aspect the invention provides isolated TLR9 polypeptides, and isolated nucleic acid molecules encoding them, from rat, pig, cow, horse, and sheep. The term "isolated" as  
10 used herein with reference to a nucleic acid molecule or polypeptide means substantially free of or separated from components with which it is normally associated in nature, e.g., other nucleic acids, proteins, lipids, carbohydrates or *in vivo* systems to an extent practical and appropriate for its intended use. In particular, the nucleic acids or polypeptides are sufficiently pure and are sufficiently free from other biological constituents of host cells so as  
15 to be useful in, for example, producing pharmaceutical preparations. Because an isolated nucleic acid or polypeptide of the invention may be admixed with a pharmaceutically acceptable carrier in a pharmaceutical preparation, the nucleic acid or polypeptide may represent only a small percentage by weight of such a preparation. The nucleic acid or polypeptide is nonetheless substantially pure in that it has been substantially separated from  
20 the substances with which it may be associated in living systems.

An amino acid sequence of rat TLR9 is provided as SEQ ID NO:1. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:1 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of rat TLR9 (See  
25 Figure 1). Amino acids numbered 1-821 of SEQ ID NO:1 are presumptively extracellular domain and correspond to SEQ ID NO:2. SEQ ID NO:3 is a nucleotide sequence of rat TLR9 cDNA having an open reading frame corresponding to nucleotides 1-3096. SEQ ID NO:4 is a nucleotide sequence of rat cDNA encoding amino acids 1-821 of SEQ ID NO:1.

An amino acid sequence of porcine TLR9 is provided as SEQ ID NO:5. Based on  
30 comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:5 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of porcine TLR9

- 8 -

(See Figure 1). Amino acids numbered 1-819 of SEQ ID NO:5 are presumptively extracellular domain and correspond to SEQ ID NO:6. SEQ ID NO:7 is a nucleotide sequence of porcine TLR9 cDNA having an open reading frame corresponding to nucleotides 77-3166. SEQ ID NO:8 is a nucleotide sequence of porcine cDNA encoding amino acids 1-819 of SEQ ID NO:5.

An amino acid sequence of bovine TLR9 is provided as SEQ ID NO:9. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:9 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of bovine TLR9 (See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:9 are presumptively extracellular domain and correspond to SEQ ID NO:10. SEQ ID NO:11 is a nucleotide sequence of bovine TLR9 cDNA having an open reading frame corresponding to nucleotides 84-3170. SEQ ID NO:12 is a nucleotide sequence of bovine cDNA encoding amino acids 1-818 of SEQ ID NO:9.

An amino acid sequence of equine TLR9 is provided as SEQ ID NO:13. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:13 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of equine TLR9 (See Figure 1). Amino acids numbered 1-820 of SEQ ID NO:13 are presumptively extracellular domain and correspond to SEQ ID NO:14. SEQ ID NO:15 is a nucleotide sequence of equine TLR9 cDNA having an open reading frame corresponding to nucleotides 115-3207. SEQ ID NO:16 is a nucleotide sequence of equine cDNA encoding amino acids 1-820 of SEQ ID NO:13.

An amino acid sequence of ovine TLR9 is provided as SEQ ID NO:17. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:17 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of ovine TLR9 (See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:17 are presumptively extracellular domain and correspond to SEQ ID NO:18. SEQ ID NO:19 is a nucleotide sequence of ovine TLR9 cDNA having an open reading frame corresponding to nucleotides 92-3178. SEQ ID NO:20 is a nucleotide sequence of ovine cDNA encoding amino acids 1-818 of SEQ ID NO:17.

- 9 -

## SEQ ID NO:1 (Rat TLR9)

MVLCRRTLHPLSLLVQAAVLAEALALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAAEPRSNITSLSLIANRI  
HHLHNLDFVHLPNVRQLNLKWNCPPLGLSPLHFSCRMTIEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLSL  
5 SHTNILLVDASSIAGLHSLRVLFDGNCYKNPCNGAVNVTPDAFLGLSNLTHLSLKYNNTLTVPRQLPPSLEYL  
LLSYNLIVKLGAEDLANLTSRMLDVGGNCRRCDHAPDLCTEQRQKSLDLHPQTFHHLHSHLEGLVLKDSLSHSLN  
SKWFQGLANLSVLDLSENFLYESINKTSFQNLTRLRKLDLSFNYCKKVSFARLHLASSFKSLVSLQELNMNGIF  
FRLLNKNTLRWLGLPKLHHTLHLQMNFINQAQLSVFSTFRALRFVDLSNNRISGPPTLSRVAPEKADEAEKGVWP  
PASLTPALPSTPVSKNFMVRCKNLRFTMDLSRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK  
10 VLDLSYNKLDLYHKSFSFSELPQLQALDLSYNSQPFMSQIGHNFSFLANLSRLQNLSLAHNDIHSRVSSRLYSTS  
VEYLDGSGNGVGRMWDEEDLYLYFFQDLRSLIHLDLSONKLHILRPQNLNLYPKSLTKLSFRDNHLSFFNWSSLA  
FLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV  
MNLTVLDVSSNPLHCACGAPFVDLLELVQTKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFGLSLL  
AVAVGTVLPLLQHLGWDVWYCFHLCCLAWPLLLTRGRRSAQALPYDAFVVFDAQSAVADWVYNELRVRLEERRG  
15 RRALRLCLEDRDWLPGQTLFENLWASTYGSRKTLFVLAHTDKVSGLLRTSFLLAQQRLLLEDRKDVVVLVILRPDA  
HRSRYVRLRQRLCRQSVLFWPHQPNGQGSFWAQLSTALTRDNHHFYNNRNFRCRGPTAE

## SEQ ID NO:2 (Rat TLR9)

MVLCRRTLHPLSLLVQAAVLAEALALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAAEPRSNITSLSLIANRI  
HHLHNLDFVHLPNVRQLNLKWNCPPLGLSPLHFSCRMTIEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLSL  
20 SHTNILLVDASSIAGLHSLRVLFDGNCYKNPCNGAVNVTPDAFLGLSNLTHLSLKYNNTLTVPRQLPPSLEYL  
LLSYNLIVKLGAEDLANLTSRMLDVGGNCRRCDHAPDLCTEQRQKSLDLHPQTFHHLHSHLEGLVLKDSLSHSLN  
SKWFQGLANLSVLDLSENFLYESINKTSFQNLTRLRKLDLSFNYCKKVSFARLHLASSFKSLVSLQELNMNGIF  
FRLLNKNTLRWLGLPKLHHTLHLQMNFINQAQLSVFSTFRALRFVDLSNNRISGPPTLSRVAPEKADEAEKGVWP  
25 PASLTPALPSTPVSKNFMVRCKNLRFTMDLSRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK  
VLDLSYNKLDLYHKSFSFSELPQLQALDLSYNSQPFMSQIGHNFSFLANLSRLQNLSLAHNDIHSRVSSRLYSTS  
VEYLDGSGNGVGRMWDEEDLYLYFFQDLRSLIHLDLSONKLHILRPQNLNLYPKSLTKLSFRDNHLSFFNWSSLA  
FLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV  
MNLTVLDVSSNPLHCACGAPFVDLLELVQTKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFG  
30

## SEQ ID NO:3 (Rat TLR9)

atgggtctctgtcgagcagccctgcacccctgtctctcctggtagcagccgcagtgctggctgaggtctctggcc  
ctgggtaccctgcctgccttctaccctgtgaactgaagcctcatggcctggtagactgcaactggctcttctctg  
aagctctgtgcctcacttctctgcccgcagaaccccggtcccaacatcaccagccttctcttgatcgccaaccgcatc  
35 caccactgcacaacctcgacttctgtccacctgcccacgtgcgacagctgaacctcaagtggaaactgtccgccc  
cctggcctcagcccttgcacttctcctgcccgcagcattgagcccaaaccttctggctatgcgcagctgtg  
gaagagctgaacctgagctataacgggtatcaccactgtgcccgcctgcccagctccctgacgaatctgagccta  
agccacaccaactcctggtagctcgatcgccagcagctcgctggcctgcacagcctgcgagttctcttcattggac  
gggaactgctactacaagaacccctgcaacggggcggtgaacgtgaccccgagcgtcttctgggcttgagcaac  
40 ctcacccacttgtcccttaagtataacaacctcacagaggtgccccgccaactgccccccagcctggagtagctc  
ctgctgtcctataacctcatcgtaagctgggggcgaagacctagccaacctgacctcccttcgaatgcttgat  
gtgggtgggaattgcccgtcgctgtgatcacgccccgacctctgtacagaatgccggcagaagtccttgatctg  
caccctcagacttctccatcacctgagccacctgaaggcctggtagctgaaggacagttctctccactcgctgaac  
tccaagtgggtccagggtctggcgaacctctcggtgctggacctgaagcgagaacttctctacgagagcatcaac  
45 aaacccagcgccttccagaacctgaccgctctgcgaagctcgacctgtccttcaattactgcaagaaggtatcg  
ttcgcccgctccactggcaagttcttcaagagcctgggtgcgctgcaggagctgaacatgaacggcatcttct  
ttcgcttactcaacaagaacacgctcaggtggctggctggctgccccagctccacacgctgcaccttcaaatg  
aatctcatcaaccaggcgcagctcagcgtctttagtaccttccgagcccttgcgttctgtggacctgtccaataat  
cgcatcagcgggctccaacgctgtccagagtcgccccgaaaaggcagacgaggcggaagggggttccatgg  
50 cctgcaagctctcaccacagctctcccgagcactcccgctctcaagaacttcatggtaggtgtaagaacctcaga  
ttcaccatggacctgtctcggaacaaccaggtgactatcaagccagagatgttcgtcaacctctccatctccag  
tgtctgagcctgagccacaactgcatcgccgaggtgtcaatggctctcagttctcgccgtgaccaacctgaag  
gtgctggacctgtcctataacaagctggacctgtaccattcgaaatcgttcagtgagctcccacagttgcaggcc

- 10 -

ctggacctgagctacaacagccagccattcagcatgcaggggatagggccacaacttcagttttctggccaatctg  
tccagggttacagaaccttagcctggcacacaatgacattcacagccgctgtcctcacgcctctacagcacctca  
gtggagtatctggacttcagcggcaacgggtgtgggcccgcagtgaggagacgtttacctctattttctc  
caagacctgagaagcctgattcatctggacctgtctcagaataagctgcacatcctccggccccagaacctcaac  
5 tacctccccaagagcctgacgaagctgagtttccgtgacaatcacctctctttctttaactggagcagctctggcc  
ttcctgcccaatctgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcaccctgcctaat  
ggcacgctcctccagaaactggatgtcagtagcaacagtatcgtctttgtgggtcccagccttctttgctctggcg  
gtagagctaaaagaggtcaacctcagccataacatcctcaagactgtggatcgctcctgggtttgggcccattgtg  
atgaacctgacgggttctagacgtgagcagcaacctctgcattgtgcctgcggtgcaccctttgtagacttactg  
10 ctggaagtgcagaccaaggtgcctggcctggcctaacgggtgtgaagtgtggcagtcctcccgccagctgcaggccgc  
agcatctttgcgcaagacctgcggctgtgcctggatgacgtcctttctcgggactgctttggcctttcactcctg  
gctgtggccgtgggacgggtgttgcctttactgcagcatctctgcggctgggacgtctgggtactgtttccatctg  
tgctggcatggctacctttgctgacctgtggcggcgacgcgccaagctctcccttatgatgccttcgtggtg  
ttcgataaggcgagagcgcggttgctgactgggtgtataacgagcttcgagtgcggttagaggagcgcgcggt  
15 cgccgagccctacgcttgtgtctggaggaccgagattggctgcctggccagacactcttcgagaacctctgggccc  
tccatctatggcagccgcaagactctgtttgtgctggccacacggaaggcagtgagcctcctgcgcaccagc  
ttcctgctggctcagcagcctgtgagcagcgtgagcagcgtggtggtgttggtgatcctgcgcctgagcc  
caccgctcccgctacgtgcgactgcgcagcgcctctgcgcagagtgctcttctggccccatcagcccaac  
gggcagggcagcttctgggcccagctgagtacagccctgactagggacaaccaccacttctataaccggaacttc  
20 tgccggggacctacagcagaatag

## SEQ ID NO:4 (Rat TLR9)

atggttctctgtcgcaggaccctgcacccttgtctctcctggtagaggccgcagtgctggctgaggctctggcc  
ctgggtaccctgcctgccttcctaccctgtgaactgaagcctcatggcctggtagactgcaactggctcttcctg  
25 aagtctgtgctcacttctctgcccagaaaccccggttccaacatcaccagcctttccttgatcgccaaccgcac  
caccacctgcacaacctcgactttgtccacctgcccacgtgcgacagctgaacctcaagtggaaactgtccgccc  
cctggcctcagcccttgcaacttctcctgcgcctgaccattgagccaaaaccttctctggtatgcgcctgctg  
gaagagctgaacctgagctataacgggtatcaccactgtgccccgcctgccagctccctgacgaatctgagccta  
agccacaccaacatcctggtactcgatgccagcagcctcgctggcctgcacagcctgcgagttctctcatggac  
30 gggaactgctactacaagaacctctgcaacggggcggtgaacgtgaccccgagccttctctgggcttgagcaac  
ctcaccacttgtcccttaagtataacaacctcacagaggtgccccgccaactgccccccagcctggagtagctc  
ctgctgtcctataacctcatcgtcaagctggggggcgaagacctagccaacctgacctcccttcgaatgcttgat  
gtgggtgggaattgcgctgcgtgtgatcacgccccgacctctgtacagaatgcgggcagaagtcccttgatctg  
caccctcagctttccatcacctgagccaccttgaggcctgggtgctgaaggacagttctctccactgcgatgac  
35 tccaagtgggtccagggtctggcgaacctctcggtgctggacctaagcgagaactttctctacgagagcatcaac  
aaaaccagcgcccttcagaacctgacctgtgcgcaagctcgacctgtccttcaattactgcaagaaggatctg  
ttcgcccgctccacctggcaagttccttcaagagcctgggtgtcgtgcagagctgaacatgaacggcatcttc  
ttccgcttactcaacaagaacacgctcaggtggctggctggctctgcccagctccacacgctgcaccttcaaatg  
aatttcatcaaccaggcgagctcagcgtctttagtaccttccgagcccttcgctttgtggacctgtccaataat  
40 cgcacagcgggctccaacgctgtccagagtcgccccgaaaaggcagacgagggcgagaaggggttccatgg  
cctgcaagtctcaccacgctctcccgagcactccgctctcaagaacttcaggtcaggtgtaagaacctcaga  
ttcaccatggacctgtctcggaacaaccagggtgactatcaagccagagatgttcgtcaacctctccatctccag  
tgtctgagcctgagccacaactgcacgcgaggtgtcaatggctctcagttcctgcgctgaccaacctgaag  
gtgctggacctgtcctataacaagctggacctgtaccattcgaaatcggttcagtgagctcccacagttgcaggcc  
45 ctggacctgagctacaacagccagccattcagcatgcaggggatagggccacaacttcagttttctggccaatctg  
tccagggttacagaaccttagcctggcacacaatgacattcacagccgctgtcctcacgcctctacagcacctca  
gtggagtatctggacttcagcggcaacgggtgtgggcccgcagtgaggagacgtttacctctattttcttc  
caagacctgagaagcctgattcatctggacctgtctcagaataagctgcacatcctccggccccagaacctcaac  
tacctcccaagagctgacgaagctgagttccgtgacaatcacctctcttctttaactggagcagctctggcc  
50 ttcttgcccaatctgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcaccctgcctaat  
ggcacgctcctccagaaactggatgtcagtagcaacagtatcgtctttgtgggtcccagccttctttgctctggcg  
gtagagctaaaagaggtcaacctcagccataacatcctcaagactgtggatcgctcctgggtttgggcccattgtg  
atgaacctgacgggttctagacgtgagcagcaacctctgcattgtgcctgcggtgcaccctttgtagacttactg  
ctggaagtgcagaccaaggtgcctggcctggcctaacgggtgtgaagtgtggcagtcctcccgccagctgcaggccgc  
55 agcatctttgcgcaagacctgcggctgtgcctggatgacgtcctttctcgggactgctttggc



- 11 -

## SEQ ID NO:5 (Porcine TLR9)

MGPRCTLHPLSLLVQVTALAAALAQGRIPAFLPCELQPHGLVNCNWLFLKSVPHFSAAAPRANVTLSLLSNRIH  
 HLHDSDFVHLSSRLTLNLKWNCPAGLSPMHFPCMTIEPNTFLAVPTLEELNLSYNSITTVPALPDSLVSLSLS  
 RTNILLVDPHTLTGLHALRYLYMDGNCYYKNPCQGALEVVPGALLGLGNLTHLSLKYNNTLEVPRSLPPSLETLL  
 5 LSYNHIVTLTPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKDHPLKHSDFSHLSRLEGLVLKDSLSYLNLD  
 RWFRGLDRLQVLDLSENFLYDCITKTTFQGLARLRLSINLSFNHYHKKVSFAHLHLAPSFGLHRLSLKELDMHGIF  
 RSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGLLYVDLSDNRISGAARPVAITREVDGRERVWLPSR  
 NLAPRPLDTLRSEDFMPNCKAFSFTLDLSRNNLVITIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVL  
 10 DLSHNKL DLYHGRSFTELPRLEALDLSYNSQPFQMVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSASLC  
 ALDFSGNDLSRMWAEGDLYLRFFQGLRSLVWLDLSQNLHTLLPRALDNLPSKSLKHLHLRDNNAFFNWSSTLL  
 PKLETDL LAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNPGFFALAKQLEELNLSANALKTVEPSWFGSMVGN  
 LKVL DVSANPLHCACGATFVGFLLEVQA AVPGPLPSRVKCGSPGQLQGHSIFAQDLRLCLDETL SWNCFGISLLAM  
 15 ALGLVVPMLHHL CGWDLWYCFHLCLAWLPHRGQRGADALFYDAFVFDKAQSAVADWVYNELRVQLEERRGRRA  
 LRLCLEERDWLPGKTLFENLWASVYSSRKTLFVLAHTDRVSGLLRASFLLAQQRLLLEDKDVVVLVILRPDAYRS  
 RYVRLRQRLCRQSVLLWPHQPRGQGSFWAQLGTALTRDNHFFYNRNFCRGPTTAE

## SEQ ID NO:6 (Porcine TLR9)

MGPRCTLHPLSLLVQVTALAAALAQGRIPAFLPCELQPHGLVNCNWLFLKSVPHFSAAAPRANVTLSLLSNRIH  
 HLHDSDFVHLSSRLTLNLKWNCPAGLSPMHFPCMTIEPNTFLAVPTLEELNLSYNSITTVPALPDSLVSLSLS  
 20 RTNILLVDPHTLTGLHALRYLYMDGNCYYKNPCQGALEVVPGALLGLGNLTHLSLKYNNTLEVPRSLPPSLETLL  
 LSYNHIVTLTPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKDHPLKHSDFSHLSRLEGLVLKDSLSYLNLD  
 RWFRGLDRLQVLDLSENFLYDCITKTTFQGLARLRLSINLSFNHYHKKVSFAHLHLAPSFGLHRLSLKELDMHGIF  
 RSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGLLYVDLSDNRISGAARPVAITREVDGRERVWLPSR  
 NLAPRPLDTLRSEDFMPNCKAFSFTLDLSRNNLVITIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVL  
 25 DLSHNKL DLYHGRSFTELPRLEALDLSYNSQPFQMVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSASLC  
 ALDFSGNDLSRMWAEGDLYLRFFQGLRSLVWLDLSQNLHTLLPRALDNLPSKSLKHLHLRDNNAFFNWSSTLL  
 PKLETDL LAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNPGFFALAKQLEELNLSANALKTVEPSWFGSMVGN  
 LKVL DVSANPLHCACGATFVGFLLEVQA AVPGPLPSRVKCGSPGQLQGHSIFAQDLRLCLDETL SWNCFG

## 30 SEQ ID NO:7 (Porcine TLR9)

gagcacgaacatccttcactgtagctgctgcccggctctgccagccagaccctttggagaagacccccactccctgt  
 catgggcccccgctgcaccctgcacccctttctctcctgggtgcaggtgacagcgctggctgcggtctctggccca  
 gggcaggctgcctgccttctgcctgtgagctccagccccagggcctggtgaactgcaactggctcttctctgaa  
 gtcctgtccccacttctcggcgccagcgccccggccacgtcaccagcctctccttactctcacaacccgcatcca  
 35 ccactgcacgactccgacttctgacacctgtccagcctacgaactctcaacctcaagtggaaactgcccgcggc  
 tggcctcagccccatgcacttccctgccacatgaccatcgagcccaacaccttctggcctgcccaccctgga  
 ggagctgaacctgagctacaacagcatcacgacgtgctgcccactccctcgtgctcctgtcgctgag  
 ccgcaccaacatcctgggtgctagacccacccacctcactggcctacatgccctgcgctacctgtacatggatgg  
 caactgctactacaagaacccctgccagggggcgctggaggtggtgccgggtgccctcctcggcctgggcaacct  
 40 cacacatctctcactcaagtacaacaatctcacggaggtgccccgcagcctgccccccagcctggagacctgtct  
 gttgtcctacaaccacattgtcacccctgacgctgaggacctggcccaatctgactgcctgcgctgcttgatgt  
 gggggggaactgcgcgcgctgtgacctgcccgcacccctgcaggagtgcccaaggaccacccccagctgca  
 ctctgacaccttcagccacctgagccgctcgaaggcctggtgttgaaagacagttctctctacaacctggacac  
 caggtggttccgaggcctggacaggtccaagtgtggacctgagtgagaacttctctacgactgcatcaccaa  
 45 gaccacggccttccagggcctggcccgactgcgcagcctcaacctgtccttcaattaccacaagaaggtgtcctt  
 tgccacctgcacctggcaccctccttgggcacctccggtccctgaaggagctggacatgcatggcatcttctt  
 ccgctcgctcagtgagaccagctccaacctctgggtccaactgcctatgctccagacctgcgctgcagatgaa  
 cttcattaaacaggcccagctcagcatctttggggccttccctggcctgctgtacgtggacctatcggaacacg  
 catcagcgagctgcgaaggccagtggccattactaggaggtggatggtaggagagggctgcgctgccttcag  
 50 gaacctcgctccacgtccactggacactctccgctcagaggacttcatgccaactgcaaggccttcagcttcac  
 cttggacctgtctcggaacaacctggtgacaatccagtcggagatgtttgctcgctctcacgcctcgagtgcct  
 gcgctgagccacaacagcatctcccaggcggtcaatggctctcagttgtgcccgtgaccagcctgcgggtgct  
 ggacctgtccacaacaagctggacctgtatcacggcgctcggttcacggagctgcgcgcctggaagcactgga  
 cctcagctacaatagccagcccttaccatgcagggtgtgggccacaacctcagcttctggtggccagctgcccgc

- 12 -

cctgcgctacctcagcctggcgcaaatgacatccatagccgagtgctccagcagctctgtagcgcctcactgtg  
cgccctggacttttagcggaacgatctgagcggatgtgggctgagggagacctctatctccgcttcttccaagg  
cctaagaagcctagtctggctggacctgtcccagaaccacctgcacacctcctgccacgtgccctggacaacct  
ccccaaaagcctgaagcatctgcatctccgtgacaataacctggccttcttcaactggagcagcctgacctcct  
5 gcccagctggaaacctggacttggctggaaaccagctgaaggccctaagcaatggcagcctgccatctggcac  
ccagctgcgaggctggacctcagtggaacagcatcggtttgtgaacctgggttcttggccctggccaagca  
gttagaagagctcaacctcagcgccaatgccctcaagacagtggagccctcctgggttggctcgatgggtgggcaa  
cctgaaagtcctagacgtgagcgccaacctctgcactgtgcctgtggggcgaccttcgtgggttctctgctgga  
10 ggtacaggctgacctgacctgggtgcccagcgcgtcaagtgtggcagtcggggcgagctccaggcccatagcat  
ctttgcgcaagacctgcgcctctgctggatgagacctctcgtggaactgttttggcatctcgtgctggccat  
ggccctgggctgggtgtgcccctgctgcaccacctctgcggctgggacctctgggtactgcttccacctgtgcct  
ggcctggctgccccaccgagggcagcgggggcgagacgcctgttctatgatgccttcgtgggtctttgacaa  
agctcagagtgctgtggcgactgggtgtacaacagctgcgggtgcagctggaggagcgccgtgggcgccgcg  
actgcgcctgtgctggaggagcgagactgggttacctggcaagacgctcttcgagaacctgtgggacctcagtcta  
15 cagcagcgcgaagacctgtttgtgctggcccacagggacctgtcagcgacctcttgctgcccagtttctctgct  
ggcccagcagcgctgctggaggaccgaaggagctgttagtgctgggtgatcctgcgccccgatgcctaccgctc  
ccgctacgtgcggctgcccagcgctctgcggcagagtgctcctcctctggccccaccagctccgctggcgagg  
cagcttctggggccagctgggacagccctgaccagggaacaaccaccttctataaccggaactctgcggggg  
ccccacgacagccgaatagcactgagtgcagccagcttgcggcagccccctggatttgctctctgctgggg  
20 tgcggccaaacctgctttgctcagccacacctgctctgctcctgttccccacccccccccagcctggcatgt  
aacatgtgccaataaatgctaccggaggggccaagaaaaaaaaaaaaaaaaa

## SEQ ID NO:8 (Porcine TLR9)

atggggccccgctgcacctgcaccccccttctctcctgggtgcaggtgacagcgctggctgcggctctggcccag  
25 ggcaggtgctgcttctcctgcccctgtgagctccagccccacggcctgggtgaactgcaactggctcttctctgaag  
tcgctgccccacttctcggcgagcgccccggccaacgtcaccagcctctccttactctccaaccgcacccac  
cacctgcacgactccgacttctgctccacctgtccagctcgaactctcaacctcaagtggaaacctccgagct  
ggcctcagccccatgcacttccccctgccacatgacctcgagcccaacaccttctggcgctgcccacctggag  
gagctgaacctgagctacaacagcatcacgacctgctgcccctgcccagctccctcgtgtccctgtcgctgagc  
30 cgcaccaacatcctggtgctagacccccaccacctcactggcctacatgcctgcgctacctgtacatggatggc  
aactgctactacaagaaccttgcaggggcgctggaggtggtgcccgggtgcccctcctcgccctgggcaacctc  
acacatctctcactcaagtacaacaatctcacggaggtgccccgcagcctgccccccagcctggagacctgctg  
tgtctcccaacacatgtgcacctgacgctgaggacctggccaatctgactgcccctgcgctgcttgatgtg  
ggggggaaactgcccgcgctgtgacctgccccgaacctctgcaactgagtgcccaaaggaccacccagctgcac  
35 tctgacaccttcagccacctgagccgctcgaaggcctgggtgtgaaagacagttctctctacaacctggacacc  
aggtgggtccgagggcctggacaggtccaagtgtggacctgagtgagaacttctctacgactgcacaccaag  
accacggccttccagggcctggcccgactgcgcagcctcaacctgtccttcaattaccacaagaaggtgtccttt  
gcccacctgcacctggcaccctcctttggggacctccggtcctgaaggagctggacatgcatggcatcttcttc  
cgctcgctcagtgagaccagctccaacctctgggtccaactgcctatgctccagacctgcgctgcagatgaac  
40 ttcattaaccagggccagctcagcatctttggggccttccctggcctgctgtacgtggacctatcggaacaaccgc  
atcagcggagctgcaaggccagtgccattactaggaggtggatggtagggagaggggtctggctgccttccagg  
aacctcgctccacgtccactggacactctccgctcagaggacttcatgcccactgcaaggccttcagcttcaacc  
ttggacctgtctcggaacaacctgggtgacaatccagtcggagatgtttgctcgctctcacgcctcgagtgcctg  
cgctgagccacaacagcatctcccaggcggtcaatggctctcagtttgtgcgctgaccagcctgcggtgctg  
45 gacctgtcccacaacagctggacctgtatcacggcgctcgttcacggagctgcccgcgctggaagcactggac  
ctcagctacaatagccagccctttaccatgcagggtgtggggccacaacctcagcttcgtggccagctgcccgcc  
ctgcgctacctcagcctggcgcaaatgacatccatagccgagtgctcccagcagctctgtagcgcctcactgtgc  
gccctggacttttagcggaacgatctgagccggatgtgggtgagggagacctctatctccgcttcttccaaggc  
ctaagaagcctagtctggctggacctgtcccagaaccacctgcacacctcctgcccagctgcccgaacctc  
50 cccaaaagcctgaagcatctgcatctccgtgacaataacctggccttcttcaactggagcagcctgacctcctg  
ccaagctggaaacctggacttggctggaaaccagctgaaggccctaagcaatggcagcctgccatctggcacc  
cagctgcggaggctggacctcagtggaacagcatcggtctttgtgaacctggcttctttggcctggccaagcag  
ttagaagagctcaacctcagcgccaatgccctcaagacagtgaggccctcctgggttggctcgatgggtgggcaac  
ctgaaagtcttagacgtgagcgccaacctctgcactgtgctgtggggcgaccttcgtgggttctctgctggag  
55 gtacaggctgcccgtgctgggtgcccagcgcgtcaagtgtggcagtcggggcgagctccaggggccatagcatc  
tttgcgcaagacctgcgcctctgctggatgagacctctcgtggaactgttttggc

- 13 -

## SEQ ID NO:9 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAEGLTLPALPCELPQPHGQVDCNWLFLKSVPHFSAAGAPRANVTSLSLISNRIH  
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTEPNTFLAVPTLEELNLSYNGITTVPALPSSSLVSLSL  
5 HTSILVLGPTHFTGLHALRFLYMDGNCYMNP CPRALEVAPGALLGLGNLTHLSLKYNNTLTVPRRLPPSLDTLL  
LSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSLSLYKLEK  
DWFRGLGRLQVLDLSENFLYDYITKTTIFNDLTQLRRLNLSFNYHKKVSFAHLHLASSFGSLVSLEKLDMHGIF  
RSLTNITLQSLTRLPKLQSLHLQLNFINQAQLSIFGAFPSLLFVDLSDNRISGAATPAAALGEVDSRVEVWRLPR  
GLAPGPLDAVSSKDFMPSCNLFNFTLDLSRNNLVTIQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLD  
10 LSHNKLDLYHGRSFTLTPQLEALDLSYNSQPFMSQGVGHNLSFVAQLPSLRYLSLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGLDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLDNLPKSLRQLRLRDNNLAFFNWSSLTVLP  
RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIPGFFVRATRLIELNLSANALKTVDPSWFGSLAGTL  
KILDVSPANPLHCACGAAFVDFLLERQEAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETSLDCFGLSLLMVA  
LGLAVPMLHHLGWDLWYCFHLCLAHLP RRRRQRGEDTLLYDAVVVFDKVQSAVADWVYNELRVQLEERRGRAL  
15 RLCLBERDWLPKLTFLFENLWASVYSSRKTMFVLDHTDRVSGLLRASFLLAQQRLLLEDKDVVVLVILRPAAYRSR  
YVRLRQLCRQSVLLWPHQPSGQGSFWANLGIALTRDNRHFYNRNFCRGPTTAE

## SEQ ID NO:10 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAEGLTLPALPCELPQPHGQVDCNWLFLKSVPHFSAAGAPRANVTSLSLISNRIH  
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTEPNTFLAVPTLEELNLSYNGITTVPALPSSSLVSLSL  
20 HTSILVLGPTHFTGLHALRFLYMDGNCYMNP CPRALEVAPGALLGLGNLTHLSLKYNNTLTVPRRLPPSLDTLL  
LSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSLSLYKLEK  
DWFRGLGRLQVLDLSENFLYDYITKTTIFNDLTQLRRLNLSFNYHKKVSFAHLHLASSFGSLVSLEKLDMHGIF  
RSLTNITLQSLTRLPKLQSLHLQLNFINQAQLSIFGAFPSLLFVDLSDNRISGAATPAAALGEVDSRVEVWRLPR  
25 GLAPGPLDAVSSKDFMPSCNLFNFTLDLSRNNLVTIQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLD  
LSHNKLDLYHGRSFTLTPQLEALDLSYNSQPFMSQGVGHNLSFVAQLPSLRYLSLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGLDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLDNLPKSLRQLRLRDNNLAFFNWSSLTVLP  
RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIPGFFVRATRLIELNLSANALKTVDPSWFGSLAGTL  
KILDVSPANPLHCACGAAFVDFLLERQEAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETSLDCFG  
30

## SEQ ID NO:11 (Bovine TLR9)

gggaagtggcgccaagcattcctgcagctgcctcccaacctgcccgccagaccctctggagaagccgcatt  
tccctgtcatggggccctactgtgccccgcaccccttctctcctgggtgcaggcgggcgactggcagcgggcc  
tgcccgagggcaccctgcctgccttccctgcctgtgagctccagcccatgggtcaggtggactgcaactggctgt  
35 tctgaagtctgtgcccgcacttttcggctggagcccccgggccaatgtcaccagcctctccttaactctccaacc  
gcatccaccacttgcatgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagtgggaactgcc  
cgccggccggcctcagcccatgcaacttccccctgcctgtatgaccatcgagcccaacaccttccctggctgtgccc  
ccctggaggagctgaacctgagctacaacggcatcacgacctgcctgcctgcctgcctgcctgcctgcctgt  
cgctgagccacaccgacatcctgggtgctaggccccaccacttcaccggcctgcacggcctgccttctgtaca  
40 tggcagggcaactgtactacatgaaccctgcggcgccctggaggtggccccaggcgccctcctcgccctgg  
gcaacctcacgcaactgtcgctcaagtacaacaacctcacggaggtgccccggcctgccccccagcctggaca  
ccctgtgtgtcctacaaccacattgtcacctggcaccggaggacctggccaacctgactgcctgcgctgtc  
ttgacgtgggtgggaactgcccgcgtgcgacctgcccgaacccctgcaggagtgcccaagaacttcccc  
agctgcacctgacaccttcagtcacctgagccgctcgaaggcctgggtgtgaaggacagttctcttacaac  
45 tagagaaagattgggtcccgccgctgggcaggctccaagtgtcgcacctgagtgagaacttctctatgactaca  
tcaccaagaccacattctcaacgacctgacccagctgcgcagactcaacctgtccttcaattaccacaagaagg  
tgtccttcgcccactgcacctagcgtcctccttgggagctcgtggtgcctggagaagctggacatgcaggca  
tcttcttcgctccctcaccaacatcacgctccagtcgctgacctggctgcccgaagctccagagtctgcatctgc  
agctgaacttcatcaaccaggccagctcagcatcttggggccttcccgagcctgtcttctgtggacctgtcgg  
50 acaaccgcatcagcggagccgcgacgccagcggccgctgggggaggtggacagcagggtggaagtctggcgat  
tgcccgaggccctcgctccaggcccgctggagccgctcagctcaaaggacttcatgccaagctgcaacctcaact  
tcaccttggaactgtcacggaacaacctgggtgacaatccagcaagagatgttaccgcctctcccgccctccagt  
gcctgcgctgagccacaacagcatctcgaggcggttaatggctcccagttcgtgcccgtgaccagcctgcgag

- 14 -

tgctcgacctgtcccacaacaagctggacctgtaccatggcgctcattcacggagctgcccagctggaggcac  
tggacctcagctacaacagccagcccttcagcatgcaggcggtgggccacaacctcagcttcgtggccagctgc  
cctccctgcgctacctcagccttgcgcacaatggcatccacagccgctgtcacagaagctcagcagcgccctgt  
tgcgcgccttgacttcagcggcaactccctgagccagatgtgggcccaggaggacctctatctctgtttttca  
5 aaggcttgaggaacctggctccagctggacctgtccgagaacctctgcacacctcctgcctcgtcacctggaca  
acctgcccagagcctgcggcagctgctctccgggacaataacctggccttcttcaactggagcagcctgaccg  
tcctgccccggctggaagccctggatctggcaggaaccagctgaaggccctgagcaacggcagcctgccgcctg  
gcacccggtccagaagctggacgtgagcagcaacagcatcggttcgtgatccccggcttcttcgtccgcgcga  
ctcggctgatagagcttaacctcagcgccaatggcctgaagacagtggatccctcctggttcggttccttagcag  
10 ggacctgaaaatcctagacgtgagcgccaacctgcctcactgcgcctgcggggcgcccttctggacttcctgc  
tggagagacaggaggccgtgccccggctgtccaggcgctcacatgtggcagtcggggccagctccaggggccgca  
gcaccttcacacaggacctgcgcctctgcctggatgagacctctccttggactgcttggcctctcactgctaa  
tgggtggcgctgggcccgtgagtgcccatgctgcaccacctctgtggctgggacctctgggtactgcttcacctgt  
gtctggcccatcttgcctcgagggcgggcgagcgggcgaggacacctgctctatgatgcctcgtggtctctcg  
15 acaagtgacagagtgcagtggtgattgggtgtacaacgagctccgcgtgcagctggaggagcgccggggcgcc  
ggcgctccgcctctgcctggaggagcagactggctccctggtaagacgctcttcgagaacctgtgggctcgg  
tctacagcagcgcaagacctgttcgtgctggaccacacggggtcagcgccctcctgcgcctcagcctatc  
tgctggccagcagcgctgttggaggaccgcaaggacgtcgtagtgctggtgatcctgcgcctcgcgcctatc  
ggctccgctacgtgcggctgcgcagcgctctgcgcagagcgctcctcctctggccccaccagccagtgggc  
20 agggtagtttctgggccaacctgggcatagccctgaccagggaacacctcactctataaccggaacttctgcc  
ggggccccacgacagccgaatagcacagagtgcctgcccag

## SEQ ID NO:12 (Bovine TLR9)

atgggccccctactgtgccccgcaccccccttctctcctgggtgcaggcgggcgacactggcagcgccctggccgag  
25 ggcacctgcctgcttccctgcctgtgagctccagccccatgggtcaggtggactgcaactggctgttctgaag  
tctgtgcgcacttttcggctggagcccccgcccaatgtcacacgcctctccttaattccaaccgcactgc  
cacttgcatgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagtggaaactgcccgccg  
ggcctcagccccatgcacttccccctgcctgatgaccatcgagcccaacaccttctggctgtgcccaacctggag  
30 gagctgaacctgagctacaacggcatcacgacctgcctgcctgcccagttccctcgtgtcctgtcgtgagc  
cacaccagcatcctggtgctaggccccaccacttcaccggcctgcacgcctgcgcttctgtacatggacggc  
aactgctactacatgaacctcctgcccgcgggcccctggaggtggccccaggcgccctcctcggcctgggcaacctc  
acgcacctgtcgtcaagtacaacaacctcacggagggtgccccgcgcctgccccccagcctggacacctgctg  
ctgtctacaaccttctgacacctggcaccggagacctggccaacctgactgcctgcgcgtgcttgacgtg  
35 ggtgggaactgcgcgcgtgcgacctgcccgaacctgcaggagtgcccaagaacttcccaagctgcac  
cctgacaccttcagtcacctgagcgccctgaaggcctgggtgtgaaggacagtctctctacaaactagagaaa  
gattggttcgcggcctgggcaggctcaaagtgtcgacctgagtgagaacttctctatgactacatcaccaag  
accaccatcttcaacgacctgacctgagctgcgcagactcaacctgtccttcaattaccacaagaagggtgctctc  
gcccacctgcacctagcgtcctccttgggagtgctggtgtcctggagaagctggacatgcacggcatcttcttc  
cgtccctcaccaacatcacgctccagtcgctgacctggctgcccagctccagagtctgcacatgcagctgaac  
40 ttcacacaccaggccagctcagcatcttggggccttcccagcctgctcttcgtggacctgtcggacaaccgc  
atcagcggagcgcgcagccagcgccgcccctgggggaggtggacagcagggtggaagtctggcgattgcccagg  
ggcctcgtccaggcccgctggacgcccgtcagctcaaaggacttcagcgaagctgcaacctcaacttcaccttg  
gacctgtcacggaacaacctgggtgacaatccagcaagagatgtttaccgcctctcccgcctccagtgctgcgc  
ctgagccacaacagcatctcgcaggcggttaatggctcccagttcgtgcccgtgaccagcctgcgagtgctcgac  
45 ctgtcccaacaagctggacctgtaccatgggcgtcattcacggagctgcccagctggaggcactggacctc  
agctacaacagccagcccttcagcatgcaggcggtggggccacaacctcagcttcgtggccagctgcccctcctg  
cgctacctcagccttgcgcacaatggcatccacagcgcgctgtcacagaagctcagcagcgctcgttgcgcgc  
ctggacttcagcggcaactcctgagccagatgtggggcgaggagacctctatctctgtcttcaaggcttg  
aggaacctggctcagctggacctgtccgagaacctatgcacacctcctgcctcgtcacctggacaacctgccc  
50 aagagcctgcccagctgcgtctccgggacaataacctggccttcttcaactggagcagcctgacctgctgccc  
cggctggaagccctggatctggcaggaaccagctgaaggccctgagcaacggcagcctgcgcctggcatccgg  
ctccagaagctggagctgagcagcaacagcatcggttcgtgatccccggcttcttcgtccgcgcgactcggctg  
atagagcttaacctcagcgccaatgcctgaagacagtggatccctcctggttcgggttccttagcagggaacctg  
aaaatcctagacgtgagcgccaacctgcctcactgcgcctgcggggcgcccttctgtggacttctgctggagaga  
55 caggaggcgtgcccggctgtccaggcgctcacatgtggcagtcggggccagctccaggggccgacatcttc  
acacaggacctgcgcctcctggatgagacctctccttggactgcttggc

- 15 -

## SEQ ID NO:13 (Equine TLR9)

MGPCHGALQPLSLLVQAAMLAVALAQGTLPFFLPCELOPHGLVNCNWLFLKSVPHFSAAPRDNVTSLSLLSNRI  
 HHLHSDFAQLSNLQKLNKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLIL  
 5 SRTNIIQLDPTSLTGLHALRFLYMDGNCYYKNPCGRALEVAPGALLGLGNLTHLSLKYNNTTVPRSLPPSLEYL  
 LLSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCVECPHKFPQLHSDTFSHLSRLEGLVLKDSLSLYQLN  
 PRWFRGLGNLTVDLSENFLYDCITKTKAFQGLAQLRRLNLSFNYHKKVSFAHLTLAPSFGLSLLSLQELDMHGIF  
 FRSLSQKTLQPLARLPMLQRLYLQMNFINQAQLGIFKDFPGLRYIDLSNDRISGAVEPVATTGEVDGGKKVWLTS  
 RDLTPGPLDTPSSEDFMPSCKNLSFTLDLSRNNLVTVQPEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQV  
 10 LDLSHNKL DLYHGRSFTLPRLEALDLSYNSQPFMRGVGHNL SFVAQLPTLRYLSLAHNGIHSRVSQQLCSTSL  
 WALDFSGNSLSQMWAEGDLYLRFFQGLRSLIRLDLSQNRLHTLLPCTLGNLPKSLQLLRRLNNYLAFNWSSLT  
 LPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRNSIIFVVPGFALATRLRELNLSANALRTEPSWFGFLAG  
 SLEVL DVSANPLHCACGA AFVDFLLQVQAAVGLPSRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFGLSLLV  
 VALGLAMPMLHHLGWDLWYCFHLGLAWLPRGWQRGADALS YDAFVVF DKAQSAVADWVYNELRVRLREERRGR  
 15 ALRLCLBERDWLPGLTFLFENLWASVYSSRKMLFVLAHTDQVSGLLRASFLLAQQRLLLEDKRDVVVLVILSPDARR  
 SRYVRLRQLRCLQSVLFWPHQPSGQRSFWAQLGMALTRDNRHFYNQNF CRGPTMAE

## SEQ ID NO:14 (Equine TLR9)

MGPCHGALQPLSLLVQAAMLAVALAQGTLPFFLPCELOPHGLVNCNWLFLKSVPHFSAAPRDNVTSLSLLSNRI  
 HHLHSDFAQLSNLQKLNKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLIL  
 20 SRTNIIQLDPTSLTGLHALRFLYMDGNCYYKNPCGRALEVAPGALLGLGNLTHLSLKYNNTTVPRSLPPSLEYL  
 LLSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCVECPHKFPQLHSDTFSHLSRLEGLVLKDSLSLYQLN  
 PRWFRGLGNLTVDLSENFLYDCITKTKAFQGLAQLRRLNLSFNYHKKVSFAHLTLAPSFGLSLLSLQELDMHGIF  
 FRSLSQKTLQPLARLPMLQRLYLQMNFINQAQLGIFKDFPGLRYIDLSNDRISGAVEPVATTGEVDGGKKVWLTS  
 25 RDLTPGPLDTPSSEDFMPSCKNLSFTLDLSRNNLVTVQPEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQV  
 LDLSHNKL DLYHGRSFTLPRLEALDLSYNSQPFMRGVGHNL SFVAQLPTLRYLSLAHNGIHSRVSQQLCSTSL  
 WALDFSGNSLSQMWAEGDLYLRFFQGLRSLIRLDLSQNRLHTLLPCTLGNLPKSLQLLRRLNNYLAFNWSSLT  
 LPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRNSIIFVVPGFALATRLRELNLSANALRTEPSWFGFLAG  
 SLEVL DVSANPLHCACGA AFVDFLLQVQAAVGLPSRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFG  
 30

## SEQ ID NO:15 (Equine TLR9)

ctctgttctctgagctgttgccgctgaaggactgagcagacaaagcatcctcctctgagctgctgccagtg  
 tgccagctggaccctctggatcatctccactcctctgcatgggcccttgccatggtgccctgagccctgtct  
 ctctggtgagcgcccatgctggcctggtctggtcccaaggcaccctgcctcctctcctgacctgtgagctc  
 35 cagccccacggcctggtgaactgcaactggctgttcttgaagtcctgctgcccacttctcagcagcagcaccg  
 gacaatgtcaccagccttctctgtctctccaaccgcatccaccactccacgactccgactttgcccactgtcc  
 aacctgcagaaactcaacctcaaatggaactgcccgcagccggcctcagccccatgcacttcccctgccacatg  
 accatcgagcccaacttctctggtgtaccacccctggaggagctgaacctgagctacaacggcatcacgact  
 gtgctgcccctgccagctcctctggtcctctgatcctgagcgcaccaacatcctgcagctagacccccaccagc  
 40 ctacgggctgcatgcccctgcgtctctatacatggatggcaactgctactacaagaacctctgccccggggcc  
 ctggaggtggccccagggcgcctccttggtctgggcaacctcaccacctgtcactcaagtacaacaacctcaca  
 acggtgccccgcagcctgccccctagcctggagtacctgctgttgcctacaaccacattgtcaccctggcacct  
 gaggacctggccaatctgactgcccctgctgtgctcgatgtgggtggaaactgcccgcgctgtgacctgacgc  
 aacctgctgctggagtggccacataaattccccagctgcaactccgacacctcagccacctaaagccgcttagaa  
 45 ggctcgtgttgaaggatagttctctctaccagctgaacccagatggttcctggtggcctgggcaacctcacagt  
 ctgcagctgagtgaagaacttctctacgactgcactaccaaaggaattccagggcctggccagctgcga  
 agactcaactgtctcttcaattaccataagaaggtgtccttcgcccacctgacgctggcaccctccttcgggagc  
 ctgctctcctctgcaggaactggacatgcatggcatctctctccgctcactcagccagaagacgctccagccactg  
 gcccgcctgcccactgctccagcgtctgtatctgcagatgaacttcatcaaccaggcccagctcgccatcttcaag  
 50 gacttccctggtctgcgctacatagacctgtcagacaaccgcatcagtgaggctgtggagccggtggccaccaca  
 ggggaggtggatggtgggaagaaggtctggtgacatccaggacactcactccaggcccactggacacccccagc  
 tctgaggacttcatgccaagctgcaagaacctcagcttcaccttgacctgtcaggaacaacctggtaacagtc  
 cagccagagatgtttgcccagctctcgccctccagtgctgctgacctgagccacaacagcatctcgaggcggtc

- 16 -

aatggctcacagttcgtgccactgaccagcctgcaggtgctggacctgtcccataacaaactggacctgtaccat  
gggcgctcgtttacggagctgcccgcgactggaggcctggacctcagctacaacagccagcccttcagcatgcgg  
gggtgsgggccacaacctcagctttgtggcccagctgccaccctgcgctacctcagcctggcacacaatggcatc  
cacagccgtgtgtcccagcagctctgcagcacctcgctgtgggcccctggacttcagcgggaattccctgagccag  
5 atgtgggctgagggagacctctatctccgcttcttccaaggcctgagaagcctaataccggctagacctgtcccag  
aatcgtctgcataccctcctgccatgcaccctgggcaacctcccgaagagcttgagctgtgcgtctccgtaac  
aattacctggccttcttcaattggagcagcctgacctcctgccaaacctggaaacctggacctggctggaac  
cagctgaaggctctgagcaatggcagcctgccttctggcaccagctccagaggctggacgtcagcaggaacagc  
atcatcttcgtggtccctggcttcttctgtctggtccacgaggtgcgagagctcaacctcagtgccaacgcctc  
10 aggacagaggagccctcctgggttgggttctcctagcaggtcccttgaaagtccctagatgtgagcgccaacctctg  
cactgcccctgtggggcagccttctgtggacttctgtctgcaggttcaggtgccgtgctggtctgccagccgc  
gtcaagtgtggcagtcggggcagctccagggcgcgagcatcttcgcacaagacctgcccctctgctggacaag  
tccctctcctgggactgttttggctctctcattgctggttgtggccctgggctggccatgctatgttgaccac  
ctctggcggtgggacctctggtactgcttccacctgggctggcctggctgcccggcggggtggcagcggggc  
15 gcgatgcccctgagctatgatgccttctgtggtcttcgacaaggcacagagcgcagtgccgactgggtgtacaat  
gaactgcgggtgcggctagaggagcgcgctgggcccggcgctccgctgtgtctggaggagcgtgactggcta  
cctggcaagagcgtgttcgaaaacctgtgggcccctcagctctacagcagccgcaagatgctgttctgtggccac  
acggaccaggtcagtgccctcttgcgtgccagcttctgtctggcccagcagcgtctgtggaggaccgcaaggac  
gttgtggtgctggtaacctgagccctgacgcccgccttccggttacgtgcggctgcgccagcgcctctgccgc  
20 cagagtgtcctctctggtcccaccagcctagtggccagcgcagcttctggggccagctaggcatggcctgacc  
agggacaaccgcccacttctataaccagaacttctgcccggggcccgacgatggctgagtagcacagagtgcagcc  
tggcatgtacaacccccagcctgacctgacctctctgcctatgatgccagctctgacctctgtgacgcccc  
tgctctgacctccgccacctcaccctggcatacagcaggcactcaataaatgccactggcaggccaaacagcca  
aaaaaaaaaaaaaaaa

25

## SEQ ID NO:16 (Equine TLR9)

atgggccccttgccatggtgcccctgcagcccctgtctctcctgggtgcaggcggccatgctggccgtggtctgtggc  
caaggcaccctgcctcccttctgcccctgtgagctccagccccacggcctggtgaactgcaactggctgttccctg  
aagtccgtgccccacttctcagcagcagcaccgggacaatgtcaccagccttctcctgtctctcaaccgcac  
30 caccacctccagcactccgactttgcccactgtccaacctgcagaaactcaacctcaaatggaactgcccggca  
gcccggcctcagcccatgcacttcccctgccacatgaccatcgagcccaacttctcctggctgtacccacctg  
gaggagctgaacctgagctacaacggcatcacgactgtgcctgccctgccagctccctcgtgtccctgatcctg  
agcgcaccaacatcctgcagctagacccaccagcctcacgggctgcatgccctgcgttccctatacatggat  
ggcaactgctactacaagaacctcgcggcgggccctggagggtggccccagggcgccctccttgccctgggcaac  
35 ctcaaccacctgtcactcaagtacaacaacctcaaacgggtgccccgcagcctgccccctagcctggagtacctg  
ctgttgcctacaaccacattgtcaccctggcacctgaggacctggccaatctgactgccctgcgtgtgctcgat  
gtgggtggaactgcccgcgctgtgaccatgcacgcaacctcctgcgtggagtggccacataaattccccagctg  
cactccgacaccttcagccacctaaagccgcttagaaggcctcggttggaaggatagttctctctaccagctgaac  
cccagatggttccgtggcctgggcaacctcacagtgctcgacctgagtgaagacttccctctacgactgcatcacc  
40 aaaaccaaggcattccagggcctggcccagctgcgaagactcaacttgtccttcaattaccataagaagggtgtcc  
ttcgcccacctgacgtggcaccctccttcgggagcctgtctccctgcaggaaactggacatgcatggcatcttc  
ttccgctcactcagccagaagacgtccagccactggccgcctgcccctgctccagcgtctgtatctgcagatg  
aacttcatcaaccaggcccagctcggtcatcttcaaggacttccctggctgtgcgtacatagacctgtcagacaac  
cgcacagtgagctgtggagcgggtggccaccacaggggaggtggatggtgggaagaaggctctggctgacatcc  
45 agggacctcactccagggccactggacccccagctctgaggacttcagtgccaagctgcaagaacctcagcttc  
accttgacctgtcacggaacaacctggtaacagtcacagccagagatggttgcccagctctcgcgctccagtg  
ctgcgctgagccacaacagcatctcgaggcggtcaatggctcacagttcgtgccactgaccagcctgcaggtg  
ctggacctgtcccataacaaactggacctgtaccatgggcgctcgtttacggagctgcccgcagctggaggccctg  
gacctcagctacaacagccagccctcagcatcggggtgtgggcccacaacctcagcttgggtggccagctgcc  
50 acctgcgctacctcagcctggcacacaatggcatccacagccgtgtgtcccagcagctctgcagcacctcgctg  
tgggcccctggacttcagcggcaattccctgagccagatgtgggctgagggagacctctatctccgcttcttccaa  
ggcctgagaagcctaataccggctagacctgtcccagaatcgtctgcataccctcctgccatgcacctgggcaac  
ctccccaaagagcttgagctgtgctcctcgtaacaattacctggccttcttcaattggagcagcctgacctc  
ctgcccacctggaaacctggacctggctggaaaccagctgaaggctctgagcaatggcagcctgccttctggc  
55 accagctccagaggctggacgtcagcaggaacagcatcatctcgtggtccctggcttcttctgtctggccacg  
aggctgcgagagctcaacctcagtgccaacgcctcaggacagaggagccctcctgggttgggttctcctagcaggc  
tcccttgaagtcctagatgtgagcgccaacctctgcactgcgctgtggggcagccttctgtgacttctgctg

- 17 -

cagggttcaggctgccgtgcctggtctgccagccgcgtcaagtgtggcagtcggggccagctccaggccgcagc  
atcttcgcacaaagacctgcccctctgctggacaagtcctctcctgggactgttttggt

## SEQ ID NO:17 (Ovine TLR9)

5 MGPYCAPHPLSLVLQAAALAAALAQGTLPALFLPCELQPRGKVCNWLFLKSVPRFSAGAPRANVTLSLSISNRIH  
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTEPNTFLAVPTLEELNLSYNGITTVPALPSSSLVLSLS  
RTSILVLGPTHFTGLHALRFLYMDGNCYYKNPCQQAQVEVAPGALLGLGNLTHLSLKYNLTFVPRRLPPSLDTLL  
LSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSLSLYKLEK  
10 DWFRGLGRLQVLDLSENFLYDYITKTTIFRNLTLQRLRLNLSFNHKKVSFAHLQLAPSFGGLVSLKLDLMHGIF  
RSLTNTTLRPLTQLPKLQSLSLQLNFINQAELSI FGAFPSLLFVDLSDNRISGAARPVAALGEVDSGVEVWRWR  
GLAPGPLAAVSAKDFMPSCNLNFTLDLSRNNLVTIQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTRLRVLD  
LSYNKLDLYHGRSFTELPQLEALDLSYNSQPFMSQGVGHNLSFVAQLPSLRYSLSLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSKNHLHTLLPRHLNLPKSLRQLRLRDNNLAFFNWSSLTVP  
15 QLEALDLAGNQLKALSNGSLPPGTRLQKLDVSSNSIGFVTPGFFVLNRLKELNLSANALKTVDPFWFGRLTETL  
NILDVSANPLHCACGAAFVDFLLEMQAAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETSLDCFGFSLLMVA  
LGLAVPMLHLHLCGWDLYCFHLCLAHLPRLRRRQRGEDTLLYDAFVVFDKAQSAVADWVYNELRVQLEERRRRAL  
RLCLEERDWPGLTFENLWASVYSSRKTMFVLDHTDRVSGLLRASFLLAQQRLLDRKDVVVLVILRPAAYRSR  
YVRLRQRLCRQSVLLWPHQPSGQGSFWANLGMALTRDNHRHFNRFNFCRGPTTAE

## 20 SEQ ID NO:18 (Ovine TLR9)

MGPYCAPHPLSLVLQAAALAAALAQGTLPALFLPCELQPRGKVCNWLFLKSVPRFSAGAPRANVTLSLSISNRIH  
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTEPNTFLAVPTLEELNLSYNGITTVPALPSSSLVLSLS  
RTSILVLGPTHFTGLHALRFLYMDGNCYYKNPCQQAQVEVAPGALLGLGNLTHLSLKYNLTFVPRRLPPSLDTLL  
LSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSLSLYKLEK  
25 DWFRGLGRLQVLDLSENFLYDYITKTTIFRNLTLQRLRLNLSFNHKKVSFAHLQLAPSFGGLVSLKLDLMHGIF  
RSLTNTTLRPLTQLPKLQSLSLQLNFINQAELSI FGAFPSLLFVDLSDNRISGAARPVAALGEVDSGVEVWRWR  
GLAPGPLAAVSAKDFMPSCNLNFTLDLSRNNLVTIQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTRLRVLD  
LSYNKLDLYHGRSFTELPQLEALDLSYNSQPFMSQGVGHNLSFVAQLPSLRYSLSLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSKNHLHTLLPRHLNLPKSLRQLRLRDNNLAFFNWSSLTVP  
30 QLEALDLAGNQLKALSNGSLPPGTRLQKLDVSSNSIGFVTPGFFVLNRLKELNLSANALKTVDPFWFGRLTETL  
NILDVSANPLHCACGAAFVDFLLEMQAAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETSLDCFG

## SEQ ID NO:19 (Ovine TLR9)

gtcggcaggggaagtgcagcgcgaagcatccttcctgcagctgccgcccacttgcccgcagaccctctggaga  
35 agccgcatttcctgccatggggccctactgtgccccgcacccctttctctcctggtgcaggcggcggtggtg  
agcagccctggccagggcaccctgctgccttcctgccctgtgagctccagccccgggtaagtgaactgcaa  
ctggtgttctgaagtctgtgcccgcgttttcggccggagccccccgggccaatgtcaccagcctctccttaat  
ctccaaccgcattccaccacttgacgactctgacttcgtccacctgtccaacctgcccgtctcaacctcaagt  
gaactgcccgcggcgccgctcagcccatgcacttcctgcccgcagcatgaccatcgagcccaacaccttcctggc  
40 tgtgcccaccctggaggagctgaacctgagctacaatggcatcacgaccgtgctgcccgtgcccagttctctcgt  
atccctgtcgctgagccgcaccagcatcctggtgctaggccccaccacttcaccggcctgcacgcccgtgccc  
tctgtacatggacggcaactgctactataagaacctgcccagcaggcctggagggtggccccaggcgcctcct  
tggcctgggcaacctcacgcacctgtcgctcaagtacaacaacctcacggaggtgccccgcgcctgccccccag  
cctggacaccctgctgctgtcctacaaccacatcatcaccctggcaccggaggacctggccaatctgactgcct  
45 gcgtgtgcttgatgtggcggggaactgccgcccgtgcgaccagcccgcgaaccttcagggagtgcccaagaa  
cttccccagctgcacctgcaccttcagccacctgagccgctcgaaggcctggtgtgaaggacagttctct  
ctacaaactagagaaagactggttccgcccgtggcagctccaagtgcctgacctgagtgagaactctctcta  
tgactacatcaccaagaccaccatcttcaggaacctgaccagctgcgcagactcaacctgtccttcaattacca  
caagaaggtgtccttcgcccacctgcaactggcaccctcctttgggggctggtgtcctggagaagctggacat  
50 gcacggcatcttctccgctccctcaccaaccacacgctccggcgctgaccagctgcccagctccagagctct  
gagctctgcagctgaacttcataaccaggccgagctcagcatcttggggccttcccagagcctgctcttcgtgga  
cctgtcggacaaccgcattcagcggagctgcgaggccggtggccgcccctggggagggtggacagcgggggtggaagt  
ctggcggtggcccaggggcctcgctccaggcccgtggccgcccgtcagcgcaaggacttcagccaagctgcaa



- 18 -

cctcaacttcaccttgacgtgtcacggaacaacctgggtgacgatccagcaggagatgtttaccgcctctcccg  
cctccagtgcctgcgcctgagccacaacagcatctcgaggcggttaatggctcgagttcgtgccgctgaccgc  
cctgcgagtgtcgcacctgtcctacaacaagctggacctgtaccatgggcgctcggtcacggagctgcgcgagct  
ggaggcactggacctcagctacaacagccagcccttcagcatgcagggcggtgggccacaacctcagcttcgtggc  
5 ctagctgccgtccctgcgtacctcagccttgcgcacaacggcatccacagccgctgtcacagaagctcagcag  
cgctcgtgcgcgcctggacttcagcggcaactccctgagccagatgtgggcccaggagacctctatctctg  
cttcttcaaaggcttgaggaacctgggtccagctggacctgtccaagaaccacctgcacacctcctgcctcgta  
cctggataacctgcccaagagcctgcgcgagctgcgtctccgggacaataacctggccttcttcaactggagcag  
cctgactgttctgccccagctggaagccctggatctggcggaaccagctgaaggccctgagcaacggcagcct  
10 gccacctggcaccggctccagaagctggacgtgagcgaacagcatcggtttgtgacctggcttcttctgt  
ccttgccaacggctgaaagagcttaacctcagcgccaacgcctgaagacagtggatcccttctgggttcggtcg  
cttaacagagacctgaatatcctagacgtgagcgccaacccgctccactgtgctgcggggcgcccttctgtga  
cttctgctggagatgcaggcgccgtgcctgggctgtccaggcgctcacgtgtggcagtcggggccagctcca  
ggggccgagcatcttcgcacaggacctgcgcctctgctggatgagacctctccttgactgcttctggcttctc  
15 gctgctaagtggcgctgggctgggctggcggtgccatgctgcaccacctctgtggctgggacctgtggtactgctt  
ccacctgtgtctggccatttgcctcgacggcgccgagcgggcgaggacacctgctctacgatgccttcgt  
ggtcttcgacaaggcgagagtgagtgccgagctgtgtacaaacagctccgctgagcctggaggagcccg  
cgggcgccggcgctccgctctgctggaggagcgagactggctccctggcaagacgctcttcgagaacctgtg  
ggcctcggtctacagcagccgtaagaccatgttctgctggaccacacggaccgggtcagtgccctcctgcgcgc  
20 cagcttctgctggcccagcagcgtgttggaggaccgcaaggatgtcgtggtgctggtgatcctgcgccccgc  
cgctaccggctccgctacgtgcggctgcgccagcgctctgcccagagagcgtcctccttgggcccaccagcc  
cagtgggccagggtagcttctgggccaacctgggcatggccctgaccagggacaaccgccacttctataaccggaa  
cttctgcgggggccccacgacagccgaatagcacagagtgaactgccag

## 25 SEQ ID NO:20 (Ovine TLR9)

atgggcccctactgtgcccgcaccccccttctctcctgggtgcaggcgggcgctggcagcagccctggcccag  
ggcaccctgectgccttctgcctgtgagctccagccccgggtaaggtgaactgcaactggctgttctgaag  
tctgtgccgcttcttgcggcgagcccccgggccaatgtcaccagcctctccttaatctccaaccgcatccac  
cacttgacgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagtggaaactgcccgccggcc  
30 ggctcagccccatgcaactccctgcgcgtgacctcgagcccaacaccttctggctgtgcccacctggag  
gagctgaacctgagctacaatggcatcacgacctgctgcccctgcccagttctctcgtatccctgtcgctgagc  
cgaccagcatcctgggtgctaggccccacccacttcaccggcctgcacgcccctgcgcttctgtacatggacggc  
aactgctactataagaaccttgcagcaggcgctggagggtggcccaggcgccctccttgccctgggcaacctc  
acgcaactgtcgctcaagtacaacaacctcagcgagggtgtccccgcgcctgccccccagcctggacacctgctc  
35 ctgtcctacaaccacatcatcaccttggcacccgaggacctggccaatctgactgcccctgcgtgtgcttgatgtg  
ggcggaactgcccgctgcgaccacgcccgaaccttgcagggagtgcccaaagaacttcccaagctgcac  
cctgacaccttcagccacctgagccgctcgaaggcctgggtgtgaaggacagtctctctacaaactagagaaa  
gactgggtccgcgccctgggaggtccaagtgtcgacctgagtgagaacttctctatgactacatcaccaag  
accaccatcttcaggaacctgaccagctgcgcgagctcaacctgtccttcaattaccacaagaagggtgtccttc  
40 gccacctgcaactggcaccctccttgggggctgggtgcccctggagaagctggacatgcacggcatcttcttc  
cgctccctcaccaacaccagctccggcgctgaccagctgcccagctccagagctgagctcgcagctgaac  
ttcatcaaccaggccgagctcagcatcttggggccttcccagacctgctctcgtggacctgtcggaacaacgc  
atcagcgagctgcgaggccggtggccgcccctcggggaggtggacagcggggtggaagtctggcggtggcccagg  
ggcctcgctccaggcccgctggccgctcagcgcaaggacttcagccaagctgcaacctcaacttcaccttg  
45 gacctgtcacggaacaacctgggtgacgatccagcaggagatgtttaccgcctctcccgcctccagtgctgcgc  
ctgagccacaacagcatctcgaggcggttaatggctcgagttcgtgcgcgtgaccgcctgcgagtgctcgac  
ctgtcctacaacaagctggacctgtaccatgggcgtcggttcacggagctgcccagctggaggcactggacctc  
agctacaacagccagcccttcagcatgcaggcgctgggcccacaacctcagcttcgtggcccagctgcgtccctg  
cgctacctcagccttgcgcacaacggcatccacagcgcggtgtcacagaagctcagcagcgctcgtcgcgcc  
50 ctggacttcagcggaacctccctgagccagatgtgggcccagggagacctctatctctgcttcttcaaaggcttg  
aggaaacctggctcagctggacctgtccaagaaccacctgcacacctcctgcctcgtcacctggataacctgccc  
aagagcctgcgcgagctgcgtctccgggacaataacctggccttcttcaactggagcagcctgactgttctgccc  
cagctggaagccctggatctggcggaaccagctgaaggccctgagcaacggcagcctgcacctggcaccgg  
ctccagaagctggagctgagcagcaacagcatcggtttgtgaccttggttcttctgcttgcacaacggctg  
55 aaagagcttaacctcagcgccaacgcctgaagacagtggatcccttctgggttcggtcgcttaacagagacctg  
aatatcctagacgtgagcgccaacccgctccactgtgctgcggggcgcccttctggacttctgctggagatg



- 19 -

caggcgccgctgacctgggctgtccaggcgctcacgtgtggcagtcggggccagctccaggcgccgagcatcttc  
gcacaggacctgacgctctgacctggatgagacctctccttgactgctttggc

Complete nucleotide and amino acid sequences for canine and feline TLR9 are publicly available. For example, an amino acid sequence for canine TLR9 is available as GenBank accession number BAC65192 and its corresponding nucleotide sequence is available as GenBank accession number AB104899. An amino acid sequence for feline TLR9 is available as GenBank accession number AAN15751 and its corresponding nucleotide sequence is available as GenBank accession number AY137581.

Complete nucleotide and amino acid sequences for canine and feline TLR9 were also determined independently from those available from public databases.

An amino acid sequence of canine TLR9 is provided as SEQ ID NO:21. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:21 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of canine TLR9 (See Figure 1). Amino acids numbered 1-822 of SEQ ID NO:21 are presumptively extracellular domain and correspond to SEQ ID NO:22. SEQ ID NO:23 is a nucleotide sequence of canine TLR9 cDNA having an open reading frame corresponding to nucleotides 91-3186. SEQ ID NO:24 is a nucleotide sequence of canine cDNA encoding amino acids 1-822 of SEQ ID NO:21.

An amino acid sequence of feline TLR9 is provided as SEQ ID NO:25. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:25 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of feline TLR9 (See Figure 1). Amino acids numbered 1-820 of SEQ ID NO:25 are presumptively extracellular domain and correspond to SEQ ID NO:26. SEQ ID NO:27 is a nucleotide sequence of feline TLR9 cDNA having an open reading frame corresponding to nucleotides 87-3179. SEQ ID NO:28 is a nucleotide sequence of feline cDNA encoding amino acids 1-820 of SEQ ID NO:25.

#### SEQ ID NO:21 (Canine TLR9)

MGPCRGALHPLSLLVQAALALALAQGTLPAPLPCELPQHLVNCNWLFLKSVPRFSAAAPRGNVTSLSLYSNRI  
HHLHDYDFVHFVHLRRLNLKWNCPASLSPMHFPCHMTIEPNTFLAVPTLEDLNLNSYNISITTVPALPSSLVSLSL  
SRTNILLVLDPATLAGLYALRFLFLDGNICYKNPCQALQVAPGALLGLGNLTHLSLKYNNLTVVPRGLPPSLEYL

- 20 -

LLSYNHIIITLAPEDLANLTALRVLDVGGNCRCDHARNPCRECPKGFQQLHPNTFGHLSHLEGLVLRDSSLSYSLD  
 PRWFHGLGNLMVLDLSENFLYDCITKTAFYGLARLRLNLSFNHKKVSFAHLHLASSFGSLLSLQELDIHGIF  
 FRSLSKTTLQSLAHLPLMLQRLHLQNLFIQAQLSIFGAFFGLRYVDLSDNRISGAAPAAATGEVEADCGERVWP  
 QSRDLALGPLGTPGSEAFMPSCRTLNFTLDLSRNNLVTVPQEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNL  
 5 RVLDSLHNKLDLYHGRSFTTELPRLEALDLSYNSQPFMSMRGVGHNLSFVAQLPALRYLSLAHNGIHSRVSQQLRSA  
 SLRALDFSGNTLSQMWAEGDLYLRFFQGLRSLVQLDLSQNLRLHTLLPRNLNLPKSLRLLRLRDNLYLAFFNWSSL  
 ALLPKLEALDLAGNQLKALSNGSLPNGTQLQRLDLSGNSIGFVVPSPFFALAVRLRELNLSANALKTVEPSWFGSL  
 AGALKVLDVDTANPLHCACGATFVDFLLEVQAAVPGLPSPRVKCGSPGQLQGRSIFAQDLRLCLDEALSWSWCFSL  
 LAVALSLAVPMLHQLCGWDLWYCFHLCLAWLPRRGRRRGVDALAYDAFVVFDAQSSVADWVYNELRVQLEERRG  
 10 RRALRLCLEERDWPVKTLFENLWASVYSSRKTFLVLARTDRVSGLLRASFLLAQORLLEDKDVVVLVILCPDA  
 HRSRYVRLRQRLCRQSVLLWPHQPSGQRSFVAQLGTALTRDNHRHFNQNFRCRGPPTA

## SEQ ID NO:22 (Canine TLR9)

MGPCRGALHPLSLLVQAAALALALAQGTLPALFLPCELQPHGLVNCNWLFLKSVPRFSAAAPRGNTLSLSYNSRI  
 15 HHLHDYDFVHFVHLRRLNLKWNCPASLSPMHFPCMTIEPNTFLAVPTLEDLNLNSYNSITTVPALPSSLSVLSL  
 SRTNILLVLDPATLAGLYALRFLFLDGNCCYKNPCQALQVAPGALLGLGNLTHLSLKYNLTVVPRGLPPSLEYL  
 LLSYNHIIITLAPEDLANLTALRVLDVGGNCRCDHARNPCRECPKGFQQLHPNTFGHLSHLEGLVLRDSSLSYSLD  
 PRWFHGLGNLMVLDLSENFLYDCITKTAFYGLARLRLNLSFNHKKVSFAHLHLASSFGSLLSLQELDIHGIF  
 20 FRSLSKTTLQSLAHLPLMLQRLHLQNLFIQAQLSIFGAFFGLRYVDLSDNRISGAAPAAATGEVEADCGERVWP  
 QSRDLALGPLGTPGSEAFMPSCRTLNFTLDLSRNNLVTVPQEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNL  
 RVLDSLHNKLDLYHGRSFTTELPRLEALDLSYNSQPFMSMRGVGHNLSFVAQLPALRYLSLAHNGIHSRVSQQLRSA  
 SLRALDFSGNTLSQMWAEGDLYLRFFQGLRSLVQLDLSQNLRLHTLLPRNLNLPKSLRLLRLRDNLYLAFFNWSSL  
 ALLPKLEALDLAGNQLKALSNGSLPNGTQLQRLDLSGNSIGFVVPSPFFALAVRLRELNLSANALKTVEPSWFGSL  
 25 AGALKVLDVDTANPLHCACGATFVDFLLEVQAAVPGLPSPRVKCGSPGQLQGRSIFAQDLRLCLDEALSWSWCF

## SEQ ID NO:23 (Canine TLR9)

aggaaggggctgtgagctccaagcatcctttcctgagctgctgcccagcctgccagccagaccctctggagaag  
 cccccgctccctgtcatgggccccctgccgtggcgccctgcaacccctgtctctcctggtgagctgcccgcgcta  
 gccctggccctggcccaggccaccctgctgcttctcctgacctgagctccagccccatggcctggtgaactgc  
 30 aactggctgttccctcaagtcctgcccccttctcctgagcctgcccccggttaacgtcaccagccttctctg  
 tactccaaccgcatccaccacctccatgactatgactttgtccacttctgccccctgccccctcaatctcaag  
 tggaaactgccccgccccgagcctcagccccatgactttcctgtcacatgaccattgagcccaacaccttctg  
 gctgtgccccaccctagaggacctgaatctgagctataacagcatcacgactgtgccccctgcccagttcgctt  
 gtgtccctgtccctgagccgcaccaacatcctggtgctggacctgccaccctggcaggcctttagccctgctg  
 35 ttctgttctcctggatggcaactgctactacaagaacccctgccagcaggccctgaggtggccccaggtgccctc  
 ctgggctgggcaacctcacacacctgtcactcaagtacaacaacctcaccgtggtgccccggggcctgcccccc  
 agcctggagtagctgtctgttctacaaccacatcatcaccctggcacctgaggacctggccaatctgactgccc  
 ctgctgttctcctgagtggtgggaactgtcgccgctgtgaccatgccccgaacccctgagggagtgccccaa  
 40 ggcttccccagctgcaccccaacaccttcggccacctgagccacctcgaaggcctggtgttgagggagagctct  
 ctctacagcctggacccccaggtggttccatggcctgggcaacctcatggtgctggacctgagtgagaacttctg  
 tatgactgcatcaccaaaacaaagccttctacggcctggccggctgctgagactcaacctgtccttcaattat  
 cataagaaggtgtcctttgccacctgcatctggcatcctccttcgggagcctactgtccctgagggagctggac  
 atacatggcatcttctccgctgctcagcaagaccagctccagtcgctggccccctgccccatgctccagcgt  
 ctgcatctgagcttgaactttatcagccaggccagctcagcatcttcggcgcccttccctggactgaggtagctg  
 45 gacttgcagacaaccgcatcagtgagctgagagcccgctgcccaggggaggtagaggcagactgtggg  
 gagagagctggtggcacagtcccggaacttctgctgggcccactgggacccccggctcagaggccttcatgccc  
 agctgcaggaccctcaacttcaccttgacctgtctcggaacaacctagtactgttcagccggagatgtttgtc  
 cggctggcgccgctccagtgctggcctgagccacaacagcatctcgagggcgtcaatggctcgagttcgtg  
 cctctgagcaacctgcccgtgctggacctgtccataacaagctggacctgtaccacgggctgcttcacggag  
 50 ctgcccgggctggaggccttgacctcagctacaacagccagcccttcagcatgccccgctgggcccacaatctc  
 agctttgtggcacagctgccagccctgctacacctcagcctggcgcaaatggcatccacagcccgctgtcccag  
 cagctccgagcgcctcgtccgggccccctggacttcagtggaataacctgagccagatgtgggcccaggaggagac  
 ctctatctccgcttctcgaaggcctgagaagcctggttcagctggacctgtccagaatcgccctgcataccctc  
 ctgccacgcaacctggacaacctccccaaagagcctgcccgtcctgcccgtccgtgacaattacctggcttcttc  
 55 aactggagcagcctggcccccttacccaagctggaagcctggacctggcggaaccagctgaaggccctgagc

- 21 -

aatggcagcttgcccaacggcaccagctccagaggctggacctcagcggcaacagcatcggtctcggtggtcccc  
 agcttttttgccctggcgtgaggtctcgagagctcaacctcagcgccaacgcctcaagacgggtggagccctcc  
 tggtttgggttccctggcgggtgccctgaaagtcctagacgtgaccgccaaccccttgcatctgcgttgcggtgca  
 5 accttcgtggacttcttgcgtggaggtgcaggctgcggtgcccggcctgcctagccgtgtcaagtgcggcagcccg  
 ggccagctccaggccgcagcatcttcgcacaggacctgcgcctctgcctggacgaagcgtctcctgggtctgt  
 ttcagcctctcgctgctggctgtggccctgagcctggctgtgcccctgctgcaccagctctgtggctgggacctc  
 tggtaactgcttccacctgtgcctggcctggctgccccggcgggggcgggcggggggtgtggatgacctggcctat  
 gacgccttcgtggtcttcgacaaggcgagagctcggtggcggaactgggtgtacaatgagctgcgggtacagcta  
 10 gaggagcgcgtggggcgccggcgttacgcctgtctggaggaaactgactgggtaccggcaaaacctcttc  
 gagaacctctgggctcagtttacagcagccgcaagacgctgtttgtgctggccgcacggacagagtacgcggc  
 ctctgctgctgacgcttctgctggcccaacagcgctgctggaggaccgcaaggacgtcggtgtgctggtgatc  
 ctgtgccccgacgcccaccgctcccgtatgtgcggctgcgccagcgctctgcgcagagctgctcctcctctgg  
 cccaccagcccagtgccagcgcagcttctgggcccagctgggcacggccctgaccagggaacacggccacttc  
 tacaaccagaacttctgcggggggccacgacagcctgataggcagacagcccagcaccttcgcgcccctacacc  
 15 ctgctgtctgtctgggatgcccagacctgctggctctacaccgcccgtctgtctccctacaccagccctggca  
 taaagcgaccgctcaataaatgctgctggtagac

## SEQ ID NO:24 (Canine TLR9)

atggggccctgcccggcgccctgcaacccctgtctcctgggtgcaggctgcgcgctagccctggccctggcc  
 20 cagggcacctgcctgccttccctgccctgtgagctccagcccatggcctgggtgaactgcaactggctgttccctc  
 aagtcggtgccccgcttctcggcagctgcaaccccggttaacgtcaccagccttctctgtactccaaccgcatc  
 caccacctccatgactatgactttgtccacttcgtccacctgcggcgctctcaatctcaagtggaaactgcccggcc  
 gccagcctcagccccatgcacttccctgtcacatgaccattgagcccaacaccttccctggctgtgcccacccta  
 gaggacctgaatctgagctataacagcatcacgactgtgcccgcctgcccagttcgctgtgtccctgtccctg  
 25 agccgcaccaacatcctgggtgctggacctgccacctggcaggccttctatgcctgaccttccctgttccctggat  
 ggcaactgctactacaagaacccctgccagcagccctgcagggtggcccaagggtgccctcctgggctgggcaac  
 ctcacacacctgtcactcaagtacaacaacctcacctgggtgcgcggggcctgccccccagcctggagtaacctg  
 ctcttgtcctacaaccacatcatcacctggcacctgaggacctggccaatctgactgcctgctgtcctcgat  
 gtgggtgggaactgtgcgcgctgtgacctgcccgttaacccctgcaggagtgccccaagggttccccagctg  
 30 caccccaacaccttcggccacctgagccacctcgaaggcctgggtgttgaggagacagctctctctacagcctggac  
 cccaggtggttccatggcctgggcaacctcatggtgctggacctgagtgaagaacttccctgtatgactgcatcacc  
 aaaaccaaagccttctacggcctggccggctgcgcgagactcaacctgtccttcaattatcataagaagggtgtcc  
 tttcccacctgcatctggcatcctccttcgggagcctactgtcctgagagctggacatatacatggcatcttc  
 ttcgctcgctcagcaagaccagctccagtcgctggcccaacctgcccagctccagcgtctgcatctgcagttg  
 35 aactttatcagccaggccagctcagcatcttcggcgcccttccctggactgcggtagctggacttgtcagacaac  
 cgcacagtgaggctgcagagcccgggctgccacaggggaggttagaggcagactgtggggagagagtctggcca  
 cagtcgccgggaccttgccttggggccactgggcacccccggctcagaggccttcatgcccagctgcaggacctc  
 aacttcaccttggaacctgtctcggaacaacctagtactgttcagccggagatgtttgtccggctggcgcgccctc  
 cagtgcctgggctgagccacaacagcatctcgagcggtcaatggctcgcagttcgtgcctctgagcaacctg  
 40 cgggtgctggacctgtccataacaagctggacctgtaccacgggcgctcgttcacggagctgcgcggctggag  
 gccttggaacctcagctacaacagccagcccttcagcatgcggggcgtgggccaacaatctcagctttgtggcacag  
 ctgccagccctgcgtacctcagcctggcgcaaatggcatccacagccgctgtccagcagctccgcagcgcc  
 tcgctccggggccctggacttctagtggaataacctgagccagatgtggggcgaggagacctctatctccgcttc  
 ttccaaggcctgagaagcctgggtcagctggacctgtccagaatcgctgcataacctcctgccacgcaacctg  
 45 gacaacctcccaagagcctgcggctcctgcggctcggtgacaattacctggctttcttcaactggagcagcctg  
 gccctcctaccaagctggaagcctggacctggcgggaaaccagctgaaggccctgagcaatggcagcttgccc  
 aacggcacccagctccagaggctggacctcagcggaacagcagcagctcggttcgtgggtccccagcttttttgcctg  
 gccgtgaggtctcgagagctcaacctcagcgccaacggcctcaagacgggtggagccctcctgggttgggtccctg  
 50 gcgggtgcccgtgaaagtcctagacgtgaccgccaaccccttgcatctgcgttgccggcgcaacctcgtggacttc  
 ttgctggaggtgcaggctgcgggtgccggcctgcctagccgtgtcaagtgcggcagccggggcagctccagggc  
 cgcagcatcttcgcacaggacctgcgcctctgcctggacgaagcgtctcctgggtctgtttcagc

## SEQ ID NO:25 (Feline TLR9)

55 MGPFCHGALHPLSLLVQAAALAVLAQGTLPAPFLPCELQRHGLVNCDWLFLKSVPHFSAAAPRGNVTSLSLSYNSRI  
 HHLHDSDFVHLSLRLRLNLKWNCPASLSPMHFPCMTIEPHTFLAVPTLEELNLSYNSITVTPALPSSLVLSLSL

- 22 -

SRTNIVLDPANLAGLSRLFLFDGNCYYKNPCPQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSLEYL  
 LLSYNHIIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCMECPKGFPHLHPDTFSLHNHLEGLVLKDSLYNLN  
 PRWFHALGNLMVLDLSENFLYDCITKTTAFQGLAQLRRLNLSFNHKKVSFAHLHLAPSFGLSLSLQQLDMHGIF  
 FRSLSETTLRLSLVHLPMLQSLHLQMFNINQAQLSIFGAFFGLRYVDLSDNRISGAMELAAATGEVDGGERVRLPS  
 5 GDALGPPGTPSSEGFMPGCKTLNFTLDLSRNNLVTIQPEMFARLSRLQCLLSRNSISQAVNGSQFMPLTSLQV  
 LDLSHNKLDLYHGRSFTTELPRLEALDLSYNSQPFMSQGVGHNLFSVAQLPALRYLSLAHNDIHSRVSQQLCSASL  
 RALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNLRLHTLLPRTLDNLPKSLRLLRLRDNYLAFFNWSSVLV  
 LPRLEALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVASSFFALATRLRELNLSANALKTVEPSWFGSLAG  
 TLKVLDVDTGNPLHCACGAAFVDFLLEVQAAVPGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCFGLSLLT  
 10 VALGLAVPMLHHLCGWDLWYCFHLCLAWLPRRGRRRGADALPYDAFVVFDAQSAVADWVYNELRVRLEERRGR  
 ALRLCLEERDNLKGLTFENLWASVYSSRKMLFVLAHTDRVSGLLRASFLLAQQRLLLEDRKDVVVLVILRPDAHR  
 SRYVRLRQRLCRQSVLLWPHQPSGQRSFVAQLGTALTRDNQHFYNQNFRCGPTTAE

## SEQ ID NO:26 (Feline TLR9)

15 MGPCGHALHPLSLVQAAALAVALAQGTLPALFLPCELQRHGLVNCDWLFLKSVPHFSAAAPRGNVTSLSLYSNRI  
 HHLHDSDFVHLSLRLNWKWNCPPASLSPMHFPCMTIEPHTFLAVPTLEELNLSYNSITVPALPSSIVLSLSL  
 SRTNIVLDPANLAGLSRLFLFDGNCYYKNPCPQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSLEYL  
 LLSYNHIIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCMECPKGFPHLHPDTFSLHNHLEGLVLKDSLYNLN  
 20 PRWFHALGNLMVLDLSENFLYDCITKTTAFQGLAQLRRLNLSFNHKKVSFAHLHLAPSFGLSLSLQQLDMHGIF  
 FRSLSETTLRLSLVHLPMLQSLHLQMFNINQAQLSIFGAFFGLRYVDLSDNRISGAMELAAATGEVDGGERVRLPS  
 GDALGPPGTPSSEGFMPGCKTLNFTLDLSRNNLVTIQPEMFARLSRLQCLLSRNSISQAVNGSQFMPLTSLQV  
 LDLSHNKLDLYHGRSFTTELPRLEALDLSYNSQPFMSQGVGHNLFSVAQLPALRYLSLAHNDIHSRVSQQLCSASL  
 RALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNLRLHTLLPRTLDNLPKSLRLLRLRDNYLAFFNWSSVLV  
 LPRLEALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVASSFFALATRLRELNLSANALKTVEPSWFGSLAG  
 25 TLKVLDVDTGNPLHCACGAAFVDFLLEVQAAVPGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCFG

## SEQ ID NO:27 (Feline TLR9)

agggctctgcgagctccaggcattctctctctgccatcgctgcccagctctgccatccagaccctctggagaagcccc  
 cactccctgtcatgggccccctgccatggcgccctgcacccctgtctctcctggtgcaggctgccgcgctggccg  
 30 tggccctggcccaggccacccctgctgctttctgcccctgtgagctccagcgccacggcctggtgaattcgact  
 ggtgttccctcaagtccgtgccccactctcggcgccagcgccccgtggtaacgtcaccagcctttccctgtact  
 ccaaccgcacccacccctccacgactccgactttgtccacctgtccagcctgcggcgctctcaacctcaaatgga  
 actgccccaccgcccagcctcagccccatgcacttccctgtcacatgaccattgagccccacaccttctgccc  
 tggccaccctggaggagctgaacctgagctacaacagcatcacgacagtaccgccccctgccagttccctcgtgt  
 35 ccctgtccttgagccgtaccaacatcctggtgctggacctgccaacctcgccagggctgcactccctgcgcttct  
 tgttccctggatggcaactgctactacaagaacccctgcccgcaggccctgcagggtggccccggcgccctccttg  
 gcctgggcaaccttacgcacctgtcactcaagtaacaacacctcactgcggtgccccgcggcctgccccccagcc  
 tggagtacctgctattgtcctacaaccacatcatcaccctggcaccctgaggacctggccaacctgaccgccccgc  
 gtgtgctcgatgtgggtgggaactgccgtcgctgtgaccacgcccgaacccctgtatggagtggcccaagggct  
 40 tcccgccacctgcacctgacaccttcagccacctgaaccacctcgaaggcctggtgttgaggagacagctctctct  
 acaacctgaaccccagatggttccatgccctgggcaacctcatggtgctggacctgagtgagaacctcctatatg  
 actgcatcaccaaaaccacagccttccaggccctggcccagctgcgcgagactcaacttgtcttcaattaccaca  
 agaagggtgctcttggccacctgcactgtggcgccctccttcgggagcctgctctccctgcagcagctggacatgc  
 atggcatcttcttccgctcgctcagcgagaccagctccggtcgctggtccacctgcccagctgcagagctctgc  
 45 acctcagatgaacttcatcaatcaggcccagctcagcatcttcggggccttccctggcctgcgatacgtggacc  
 tgtcagacaacccataagtggagccatggagctggcggtgccacgggggaggtggatgggtggggagagagctcc  
 ggctgccatctggggacctagctctgggcccaccgggacccttagctccgagggttcatgccaggctgcaaga  
 ccctcaacttcaccttggacctgtcacggaacaacctagtgaacatccagccagagatggttggccggctctcgc  
 gcctccagtgctgctcctgagccgcaacagcatctcgaggcagtcacaggctcacaatttatgccgctgacca  
 50 gcctgcagggtgctggacctgtccataacaagctggacctgtaccatggcgctcttccagggagctgcccgggc  
 tggaggccctggacctcagctacaacagccagcccttcagcatgcaggcgctgggtcacaacctcagcttctgtg  
 cacagctgcgggcccctgcgctatctcagcctggcgccacacagatccacagccgtgtgtccagcagctctgca  
 gcgctcgctgcgggcccctggacctcagcggaatgcttgcggagctgtggggcgaggagacctgtatctcc  
 actcttccgagccctgaggagcctggctcggttgatctgtccagaatcgctgcataacctcttgcacgca  
 55 ccctggacaacctccccagagcctgcggctgctgcgctctccgtgacaattatctggcttcttcaactggagca

- 23 -

gcttggtcctcctccccaggctggaagccctggacctggcgggaaaccagctgaaggccctgagcaacggcagct  
 tgcctaattggaaccagctccagaggctggacctcagcagcaacagtatcagcttcgtggcctccagcttttttg  
 ctctggccaccaggctgagagctcaacctcagtgccaacgccctcaagacggaggagccctcctgggtcggtt  
 ctctagcgggcaccctgaaagtcttagatgtgactggcaacccctgactgcgcctgtggggcgccctcgtgg  
 5 acttcttgctggaggctgaggtgcaggtgcagtgcccggcctgccaggccacgtcaagtgtggcagtcaggcagctcc  
 agggccgcagcatctttgcgaggatctgcgccctctgctggatgaggccctctcctgggactgttttgccctct  
 cgtgctgaccgtggccctggcctggcctgcccagctgctgaccacctctgtggctgggacctctgggtactgct  
 tccacctgtgcttgccctggctgcccggcgggggcgggcgggcgggcgggatgcccctgacctacgatgaccttg  
 tggctcttcgacaaggcacagagcgcggtggccgactgggtgtacaacagagctgcggttacggctagaggagcgcc  
 10 gtggacgcgagcgctccgctgtgctggaggaaactgactggctaccgggtaaaacgctctttgagaacctgt  
 gggcctcagtttacagcagccgaagatgctgtttgtgctggcccacacagacagggtcagcgccctcttgcgcg  
 ccagctttctgctggcccagcagcgccctgctggaggaccgcaaggacgttgtgtgtgctgggtgatcctgccccg  
 acgcccaccgctcccgtatgtgcggtgctgcccagcgccctctgcccagagcgctcctcctctggccccaccagc  
 ccagtgggcagcgagcttctggggccagctgggcacggccctgaccagggaacaaccagcacttctataaccaga  
 15 acttctgcccggggcccccacgacggcagagtgaccgcccagcaccccaagcctcctacacctgacctgtctgacctg  
 ggatgcccggg

## SEQ ID NO:28 (Feline TLR9)

atgggcccctgccatggcgccctgcaccccctgtctcctcgttgaggtgcgcgctggccgtggccctggcc  
 20 cagggcaccctgcctgcctttctgccctgtgagctccagcgccacggcctgggtgaattgcgactggctgttcctc  
 aagtccgtgccccacttctcgccggcagcgccccgtggtaacgtcaccagcctttccctgtactccaaccgcatc  
 caccacctccacgactccgactttgtccacctgtccagcctgcggtctcaacctcaaatggaactgccacccc  
 gccagcctcagccccatgcacttcccctgtcacatgaccattgagccccacaccttccctggcgtgcccaccctg  
 gaggagctgaacctgagctacaacagcatcacgacagtaaccgcccctgccagttccctcgtgtccctgtccttg  
 25 agcgtaccacatcctgggtgctggacctgccaacctcgcagggtgcactccctgcgctttctgttccctggat  
 ggcaactgctactacaagaacccctgcccgcagccctgaggtggccccggcgccctccttggcctgggcaac  
 cttacgcacctgtcactcaagtacaacaacctcactgcggtgccccggcgccctgccccccagcctggagtaactg  
 ctattgtcctacaaccacatcatcacctggcacctgaggacctggccaacctgaccgcccctgcgtgtgctcgat  
 gtgggtgggaactgcccgtgctgtgaccacgcccgaacccctgtatggagtggcccaagggttcccgacctg  
 30 caccctgacaccttcagccacctgaaccacctcgaaggcctgggtgtgaaggacagctctctacaacctgaac  
 ccagatgggtccatgcccctgggcaacctcatgggtgctggacctgagtgaagaacttccatatactgactgcatcacc  
 aaaaccacagccttccaggccctggcccagctgcccagactcaacttgtctttcaattaccacaagaagggtgtcc  
 ttgcccacctgcatctggcgcctccttcgggagcctgctcctcctgcagcagctggacatgcatggcatcttc  
 35 ttcgctcgctcagcgagaccacgctccggtcgctgggtccacctgcccagctgcccagctgcccagctgcccagctg  
 aacttcatcaatcaggcccagctcagcatcttcggggccttccctggcctgcgatacgtggacctgacagacaac  
 cgcataagtggagccatggagctggcggtgcccagggggaggtggatgggtggggagagagtcgggctgccatct  
 ggggacctagctctggggccaccggggcaccctagctccgagggttcatgccaggctgcaagacctcaacttc  
 accttggacctgtcacggaacaacctagtgaacaatccagccagagatgtttgcccggctctcgcgctccagtgc  
 ctgctcctgagccgcaacagcatctcgcaggcagtcacggctcacaatttatgcccgtgaccagcctgcaggtg  
 40 ctggacctgtcccataacaagctggacctgtaccatgggcgctctttcacggagctgcccgggctggaggccctg  
 gacctcagctacaacagccagcccttcagcatgcaggcgctgggtcacaacctcagctttgtggcacagctgccc  
 gccctgcgctatctcagcctggcgacacacgacatccacagcgtgtgtcccagcagctctgcagcgccctcgctg  
 cgggcttggacttcagcggaatgccttgagccggatgtggggcgaggagacctgtatctccacttcttccga  
 ggctgaggagcctgggtccggttgatctgtccagaatcgctgcataacctcttgccacgcacctggacaac  
 45 ctccccaagagcctgcggctgctgctcctgtgacaattatctggctttcttcaactggagcagcctggctctc  
 ctcccgagctggaagccctggacctggcgggaaaccagctgaaggccctgagcaacggcagcttgccataatgga  
 accagctccagaggctggacctcagcagcaacagtatcagcttcgtggcctccagctttttgtcttgccacc  
 aggtgcgagagctcaacctcagtgccaacgccctcaagacgggtggagccctcctgggttcggttctctagcgggc  
 acctgaaagtcttagatgtgactggcaacccctgcagctgcgctgtggggcgccctctgagacttctgtgctg  
 50 gaggtgcaggctgcagtgcccggcctgccaggccacgtcaagtgtggcagtcaggctcaggggccgcagc  
 atctttgcgcaggatctgcgctctgctggatgaggccctctcctgggactgttttggc

Complete nucleotide and amino acid sequences for murine and human TLR9 are publicly available. For example, an amino acid sequence of murine TLR9 is available as

- 24 -

GenBank accession no. AAK29625, provided as SEQ ID NO:29. Amino acids numbered 1-821 of SEQ ID NO:29 presumptively include the entire extracellular domain and correspond to SEQ ID NO:30. SEQ ID NO:31 corresponds to GenBank accession number AF348140, which is a nucleotide sequence of murine TLR9 cDNA. SEQ ID NO:32 is a nucleotide sequence of murine cDNA encoding amino acids 1-821 of SEQ ID NO:29.

An amino acid sequence of human TLR9 is available as GenBank accession no. AAF78037, provided as SEQ ID NO:33. Amino acids numbered 1-820 of SEQ ID NO:33 presumptively include the entire extracellular domain and correspond to SEQ ID NO:34. SEQ ID NO:35 corresponds to GenBank accession number AF245704, which is a nucleotide sequence of human TLR9 cDNA. SEQ ID NO:36 is a nucleotide sequence of human cDNA encoding amino acids 1-820 of SEQ ID NO:33.

#### SEQ ID NO:29 (MURINE TLR9)

```

15 MVLRRRTLHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAASCSNITRLSLISNRI
HHLHNSDFVHLSNLRQLNLKWNCPPTGLSPLHFSCHMTIEPRTFLAMRTLEELNLSYNGITTVPRLPSSLVNL
SHTNILLVLDANSLAGLYSLRVLFMDGNCYKPNCTGAVKVTPGALLGLSNLTHLSLKYNNTKVPRQLPPSLEYL
LVSYNLIVKLGPEDLANLTSLRVLDVGGNCRCDHAPNPCIECGQKSLHLHPETFHHLSHLEGLVLKDSSSLHTLN
20 SSWFQGLVNLVLDLSENFLYESINHNAFQNLTRLRKLNLNLSFNRYKKVSFARLHLASSFKNLVSLQELNMNGIF
FRSLNKYTLRWLADLPKLHTLHLQMNFINQAQLSIFGTFRALRFVDLSNRIISGPSTLSEATPEEADDAEQEELL
SADPHAPLSTPASKNFMDRCKNFKFTMDLSRNNLVTIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ
VLDLSHNKLDLYHWKSFSELPQLQALDLSYNSQPFMSKGIHNFVSFVAHLSMLHSLSLAHNDIHTRVSSHLSNS
VRFLDFSGNGMGRMWDEGGLYLHFFQGLSGLLKLKDLSDNNLHILRPQNLNLPKSEKLLSLRDNYLSFFNWTSL
FLPNLEVLDLAGNQLKALTNGTLPNGTLLQKLDVSSNSIVSVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV
25 MNLTVDLVRNPLHCACGAADFVLDLLEVQTKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFGLSL
AVAVGMVVPILHHLCGWDVWYCFHLCLAWLPLILARSRSQAALPYDAFVFDKAQSAVADWVYNELRVRLERRG
RRALRLCLEDRDWLPGQTLFENLWASIYGSRKTLFVLAHTDRVSGLLRTSFLLAQQRLLDRKDVVVLVILRPDA
HRSRYVRLRQLCRQSVLFWPQQPNGQGFWAQLSTALTRDNHRHFYNQNFRCGPTAE

```

#### SEQ ID NO:30 (MURINE TLR9)

```

30 MVLRRRTLHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAASCSNITRLSLISNRI
HHLHNSDFVHLSNLRQLNLKWNCPPTGLSPLHFSCHMTIEPRTFLAMRTLEELNLSYNGITTVPRLPSSLVNL
SHTNILLVLDANSLAGLYSLRVLFMDGNCYKPNCTGAVKVTPGALLGLSNLTHLSLKYNNTKVPRQLPPSLEYL
LVSYNLIVKLGPEDLANLTSLRVLDVGGNCRCDHAPNPCIECGQKSLHLHPETFHHLSHLEGLVLKDSSSLHTLN
35 SSWFQGLVNLVLDLSENFLYESINHNAFQNLTRLRKLNLNLSFNRYKKVSFARLHLASSFKNLVSLQELNMNGIF
FRSLNKYTLRWLADLPKLHTLHLQMNFINQAQLSIFGTFRALRFVDLSNRIISGPSTLSEATPEEADDAEQEELL
SADPHAPLSTPASKNFMDRCKNFKFTMDLSRNNLVTIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ
VLDLSHNKLDLYHWKSFSELPQLQALDLSYNSQPFMSKGIHNFVSFVAHLSMLHSLSLAHNDIHTRVSSHLSNS
VRFLDFSGNGMGRMWDEGGLYLHFFQGLSGLLKLKDLSDNNLHILRPQNLNLPKSLKLLSLRDNYLSFFNWTSL
40 FLPNLEVLDLAGNQLKALTNGTLPNGTLLQKLDVSSNSIVSVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV
MNLTVDLVRNPLHCACGAADFVLDLLEVQTKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFG

```

#### SEQ ID NO:31 (MURINE TLR9)

```

tgtcagagggagcctcgggagaatcctccatctcccaacatggttctcgcgcgaaggactctgcaccccttgctcc
ctcctggtacaggctgcagtgcctggctgagactctggccctgggtaccctgcctgccttcctaccctgtgagctg

```

- 25 -

aagcctcatggcctgggtggactgcaattggctgttctcctgaagtctgtaccccggtttctctgcgccagcatcctgc  
tccaacatcaccgcctctccttgatctccaaccgtatccaccacctgcacaactccgacttcgtccacctgtcc  
aacctgcgccagctgaacctcaagtgggaactgtccaccactggccttagccccctgcacttctcttgccacatg  
accattgagccagaaccttctcctgggtatgctgactggaggagctgaacctgagctataatgggtatcaccact  
5 gtgccccgactgcccagctccctgggtgaatctgagcctgagccacaccaacatcctgggttctagatgctaacagc  
ctcgccggcctatacagcctgcgcgttctcttcatggacgggaactgtactacaagaacccctgcacaggagcg  
gtgaaggtgacccaggcgccctcctgggcctgagcaatctcaccatctgtctctgaagtataacaacctcaca  
aaggtgccccgccaactgccccccagcctggagtacctcctgggtgtcctataacctcattgtcaagctggggcct  
gaagacctggccaatctgacctcccttcgagtagtctgagtggtgggaattgcgctgctgcgacctgcccc  
10 aatccctgtatagaatgtggccaaaagtcctccacctgcacctgagacctccatcacctgagccatctggaa  
ggcctgggtgtgaaggacagctctctccatacactgaactcttccctgggtccaaggtctggtaacctctcggtg  
ctggacctaaagcgagaacttctctatgaaagcatcaaccacaccaatgcctttcagaacctaaaccgcctgcgc  
aagctcaacctgtccttcaattaccgcaagaaggtatcctttgccccctccacctggcaagttccttcaagaac  
ctgggtgctactgcaggagctgaacatgaacggcacttcttccgctcgctcaacaagtacacgctcagatggctg  
15 gccgatctgccccaaactccacactctgcactcttcaaatgaacttcatcaaccaggcacagctcagcatcttgggt  
accttccgagcccttcgcttctgtggacttctcagacaatcgcatcagtgggccttcaacgctgtcagaagccacc  
cctgaagaggcagatgatgcagagcaggaggagctgtgtctgcggtacctcaccagctccactgagcaccct  
gcttctaagaacttcatggacaggtgtaagaacttcaagttcaccatggacctgtctcggaacaacctgggtgact  
atcaagccagagatgtttgtcaatctctcagcctccagtgcttagcctgagccacaactccattgacaggct  
20 gtcaatggctctcagttcctgcccgtgactaatctgcaggtgctggacctgtcccatacaaaactggacttgtac  
cactggaaatcggtcagtgagctaccacagttgcaggccctggacctgagctacaacagccagccctttagcatg  
aagggtataggccacaaatttcagtttctgtggcccatctgtccatgctacacagccttagcctggcacacaatgac  
attcatacccggtgtgtcctcacatctcaacagcaactcagtgaggttcttgcacttcagcggaacgggtatgggc  
cgcatgtgggatgaggggggcttctctccatttcttccaaggcctgagtgccctgctgaagctggacctgtct  
25 caaaataacctgcatatcctccggccccagaacctgacaacctccccagagcctgaagctgctgagcctccga  
gacaactacctatcttcttcaactggaccagctctgtccttccctgcccaacctgggaagtcctagacctggcaggc  
aaccagctaaaggccctgaccaatggcaccctgcctaattggcaccctcctccagaaactggatgtcagcagcaac  
agtatcgtctctgtgggtcccagccttcttccgtctggcggtcgagctgaaagaggtcaacctcagccacaacatt  
ctcaagacggtggatcgctcctgggttggggcccatctgtgatgaacctgacagttctagacgtgaaagcaacct  
30 ctgcactgtgcctgtggggcagccttcgttagacttactgttgagggtgcagaccaggtgcctggcctggtaaat  
gggtgtgaagtgtggcagccccggccagctgcagggccgtagcatcttcgcacaggacctgcggctgtgcctggat  
gaggtcctctcttgggactgcttggcccttctactcttggctgtggccgtgggcatgggtaccttcttggccccgagccga  
catctctgcggctgggacgtctggtaactgttttcatctgtgcctggcatgggtaccttcttggccccgagccga  
cgcagcgcccaagctctccctatgatgccttcgtgggtgttcgataaggcacagagcgcagttgaggactgggtg  
35 tataagagctgccccgtgccccggaggagcgccggtcgccgagccctacgcttgtgtctggaggaccagat  
tgggtgcctggccagagcctcttcgagagcctctgggcttccatctatgggagccgcaagactctatttgtgctg  
gcccacacgggacgcgtcagtgccctcctgcgcacagcttccctgctggctcagcagcgctgttggaaagccgc  
aaggacgtgggtgtgtgtgatcctgcgtccggatgccaccgctcccgtatgtgcgactgcgcagcgtctc  
tgccgccagagtggtctcttctggccccagcagcccaacgggcaggggggttcttggggccagctgagtagacc  
40 ctgactagggaacaaccgccactctataaccagaacttctgcccgggacctacagcagaatagctcagagcaaca  
gctggaaacagctgcactctcatgcctgggtcccgagttgctctgcctgc

## SEQ ID NO:31 (Murine TLR9)

atgggttctccgtcgaaggactctgcacccttgtccctcctggtagaggtgcagtgctggctgagactctggcc  
45 ctgggtaccctgcctgccttccctaccctgtgagctgaagcctcatggcctgggtggactgcaattggctgttccgtg  
aagctgtaccgccgttctctcgccgagcatcctgtcccaacatcaccgcctctccttgatctccaaccgtatc  
caccacctgcacaactccgacttcgtccacctgtccaacctgcggcagctgaacctcaagtggaaactgtccacc  
actggccttagccccctgcacttctcttgccacatgaccattgagcccgagaaccttccctggctatgcgtacatg  
50 gaggagctgaacctgagctataatgggtatcaccactgtgccccgactgccagctccctgggtgaatctgagcctg  
agccacaccaacatcctgggtcttagatgctaacagcctcgccggcctatacagcctgcgcgttctcttcatggac  
gggaactgctactacaagaacccctgcacaggagcggtgaaggtgaccccgagcgccctcctgggcctgagcaat  
ctcaccatctgtctctgaagtataacaacctcacaagggtgccccgccaactgccccagcctggagtacctc  
ctgggtgctctataacctcattgtcaagctggggcctgaagacctggccaatctgacctcccttcgagtagcttgat  
gtgggtgggaattgcgctgcgtgcgacctgcccccaacctctgtatagaatgtggccaaaagtcctccacctg  
55 caccctgagaccttccatcacctgagccatctggaaggcctgggtgctgaaggacagctctctccatacactgaac  
tcttctgggttccaaggtctgggtcaacctctcggtgctggacctaaagcgagaacttctctatgaagcatcaac  
cacaccaatgcctttcagaacctaaaccgcctgcgcaagctcaacctgtccttcaattaccgcaagaaggtatcc



- 26 -

tttgcccgcctccacctggcaagttccttcaagaacctgggtgtcactgcaggagctgaacatgaacggcatcttc  
 ttcgcgtcgctcaacaagtacacgctcagatggctggcgcgatctgcccactccacactctgcatcttcaaatg  
 aacttcatcaaccaggcacagctcagcatctttgggtaccttccgagcccttcgctttgtggacttgtcagacaat  
 5 cgcacatcagtgggccttcaacgctgtcagaagccaccctgaagaggcagatgatgcagagcaggaggagctgttg  
 tctgcggtatcctcaccagctccactgagcaccctgcttctaagaacttcatggacaggtgtaagaacttcaag  
 ttcacatggacgtgtctcggaacaacctgggtgactatcaagccagagatgtttgtcaatctctcacgcctccag  
 tgtcttagcctgagccacaactccattgcacaggctgtcaatggctctcagttcctgcccgtgactaatctgcag  
 gtgctggacctgtcccataacaaactggacttgtaccactggaaatcgttcagtgagctaccacagttgcaggcc  
 ctggacctgagctacaacagccagcccttttagcatgaagggtataggccacaatttcagttttgtggcccatctg  
 10 tccatgctacacagccttagcctggcacacaatgacattcataccctgtgtctcacatctcaacagcaactca  
 gtgaggtttcttgacttcagcggcaacggatgtggccgcgatgtgggatgaggggggctttatctccatttcttc  
 caaggcctgagtgccctgtgaagctggacctgtctcaaaataacctgcatactctccggccccagaaccttgac  
 aacctccccaagagcctgaagctgtgagcctccgagacaactacctatcttctttaactggaccagctctgtcc  
 ttctgcccacctggaagtcctagacctggcaggcaaccagctaaaggccctgaccaatggcaccctgccta  
 15 ggcacctctccagaaactggatgtcagcagcaacagatctcgtctctgtgtggtcccagccttcttcgctctggcg  
 gtcgagctgaaagctcaacctcagccacacacattctcaagacggtggatcgctcctgggtttgggcccattgtg  
 atgaacctgacagttctagacgtgagaagcaacctctgcactgtgctgtggggcagccttcgtgacttactg  
 ttggaggtgcagaccaaggtgcctggcctggctaattggtgtgaagtgtggcagccccggccagctgcaggccgt  
 agcatcttcgcacaggacctgcggctgtgacctgaggtcctctcttgggactgctttggc  
 20

## SEQ ID NO:33 (Human TLR9)

MGFCRSALHPLSLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRI  
 HHLHDSDFAHLPRLRLNLKWNCPVGLSPMHFPCMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSL  
 25 SHTNIMLMLDSASLAGLHALRFLFMDGNCYKNPCRQALEVAPGALLGLNLTHLSLKYNNTLVVPRNLPSSLEYL  
 LLSYNRIVKLAPEDLANLTALRVLDVGGNCRCDHAPNCPMECPRHFPQLHPDTFSLSLRLEGLVLKDSLSWLN  
 ASWFRGLGNLRVLDLSENFYKCIITKFAFQGLTQLRKLNLSFNQKRVSAHLSLAPSFGLVALKELDMHGIF  
 FRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVLDSDNRISGASELTATMGEADGGEKVWLQ  
 GD LAPAPVDTPSSEDFRPNCTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV  
 LDLSRNKLDLYHEHSFTELPRLEALDLSYNSQPFMGQGVGHNFSAHLRLTLRHLSLAHNNIHSQVSQQLCSTSL  
 30 RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNRHLTLPLQTLRLNLPKSLQVLRRLRDNYLAFFKWWSLHF  
 LPKLEVLDLAGNRLKALTNGSLPAGTRLRLDVSNCNISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLAS  
 ALQILDVSPANPLHCACGAAMDFLLEVQAAPVGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCAFSLLA  
 VALGLGVPMHLHLCGDLWYCFHLCLAWLPWRGRQSGRDEALPYDAFVFDKTQSAVADWVYNELRGQLEECRG  
 RWALRLCLEERDWPGLKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLAQQRLLEDKDVVVLVILSPDG  
 35 RRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHFFYNRNFQGPAT

## SEQ ID NO:34 (Human TLR9)

MGFCRSALHPLSLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRI  
 HHLHDSDFAHLPRLRLNLKWNCPVGLSPMHFPCMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSL  
 40 SHTNIMLMLDSASLAGLHALRFLFMDGNCYKNPCRQALEVAPGALLGLNLTHLSLKYNNTLVVPRNLPSSLEYL  
 LLSYNRIVKLAPEDLANLTALRVLDVGGNCRCDHAPNCPMECPRHFPQLHPDTFSLSLRLEGLVLKDSLSWLN  
 ASWFRGLGNLRVLDLSENFYKCIITKFAFQGLTQLRKLNLSFNQKRVSAHLSLAPSFGLVALKELDMHGIF  
 FRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVLDSDNRISGASELTATMGEADGGEKVWLQ  
 GD LAPAPVDTPSSEDFRPNCTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV  
 45 LDLSRNKLDLYHEHSFTELPRLEALDLSYNSQPFMGQGVGHNFSAHLRLTLRHLSLAHNNIHSQVSQQLCSTSL  
 RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNRHLTLPLQTLRLNLPKSLQVLRRLRDNYLAFFKWWSLHF  
 LPKLEVLDLAGNRLKALTNGSLPAGTRLRLDVSNCNISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLAS  
 ALQILDVSPANPLHCACGAAMDFLLEVQAAPVGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCA

## 50 SEQ ID NO:35 (Human TLR9)

aggctgggtataaaaaatcttacttctctattctctgagccgctgctgcccctgtgggaagggaacctcgagtgtga  
 agcatccttccctgtagctgctgtccagctctgcccgcagaccctctggagaagccctgccccccagcatgggt  
 ttctgcccgcagcgcctgcaccgctgtctctcctggtgcaggccatcatgctggccatgacctggccctgggt



- 27 -

accttgccctgccttcctaccctgtgagctccagccccacggcctggtgaactgcaactggctgttcctgaagtct  
 gtgccccactttctccatggcagcaccctgtggcaatgtcaccagcctttccttgctcctccaaccgcatccaccac  
 ctccatgattctgactttgcccacctgcccagcctgcccagctctcaacctcaagtggaaactgcccgcgggttggc  
 ctgagccccatgcacttcccctgccacatgaccatcgagcccagcacttcttggtgtgcccaccctggaagag  
 5 ctaaactgagctacaacaacatcatgactgtgcctgcgctgcccacaaatccctcatatccctgtccctcagccat  
 accaaccatcctgatgctagactctgcccagcctgcgcggcctgcatgcccctgcgcttctattcatggacggcaac  
 tgttattacaagaacccctgcaggcaggcactggaggtggccccgggtgcccctccttgccctgggcaacctcacc  
 cacctgtcactcaagtacaacaacctcactgtggtgccccgcaacctgccttccagcctggagtatctgctgtg  
 tccataaacgcgcatcgtcaaacctggcgccctgaggacctggccaatctgaccgcccctgcgtgtgctcgatgtgggc  
 10 ggaaattgcccgcgctgcgaccagctcccaacccctgcatggagtcccctcgtcacttccccagctacatccc  
 gataccttcagccacctgagcgtcttgaaggcctgggtgttgaaggacagttctctctcctggctgaatgccagt  
 tgggtccgtgggctgggaaacctccgagtgctggacctgagtgagaacttctctacaaatgcatcactaaaacc  
 aaggccttccagggcctaacacagctgcgcaagcttaacctgtccttcaattacaaaaagagggtgtcctttgcc  
 cacctgtctctggccccttccctcggggagcctggtgcgcctgaaggagctggacatgcacggcatcttcttccgc  
 15 tcatcgatgagaccagctccggccactggccgcctgcccactgctccagactctgcgtctgcagatgaacttc  
 atcaaccaggcccagctcgcatcttccaggccttccctggcctgcgtacgtggacctgtcggaacaaccgcatc  
 agcggagcttccggagctgacagccaccatgggggaggcagatggaggggagaaggctctggtgcagcctggggac  
 cttgctccggccccagtggaactcccagctctgaagacttcaggcccaactgcagcaccctcaacttcaccttg  
 gatctgtcacggaacaacctggtagcctgcagccggaatgtttgcccagctctcgcacctgcagtgccctgcgc  
 20 ctgagccacaactgcatctcgcaggcagtcacatggctcccagttcctgccgtgaccggtctgcaggtgctagac  
 ctgtcccgaataagctggacctctaccacgagcactcattcacggagctaccgcgactggagggcctggacctc  
 agctacaacagccagcccttggcatgcaggcgtggggccacaactcagcttctggtgctcacctgcgcaccctg  
 cgccacctcagcctggcccaacaacatccacagccaagtgtcccagcagctctgcagtacgtcgctgcgggccc  
 ctggacttcagcggcaatgcactggggccatgtgtggccgagggagacctctatctgacttcttccaaggcctg  
 25 agcgggttgatctggctggactgtcccagaaccgctgcacacctcctgcccacaaacctgcgcaacctcccc  
 aagagcctacaggtgctgcgtctccgtgacaattacctggccttctttaagtgggtggagcctccacttccctgcc  
 aaactggaaagtccctgcacctggcaggaacccggctgaaggccctgaccaatggcagcctgcctgctggcaccgg  
 ctccggaggtctggatgtcagctgcaacagcatcagcttctggtggcccccggttcttttccaaggccaaggagctg  
 cgagagctcaaccttagcgccaacgcccctcaagacagtggaccactcctgggttggggcccctggcgagtgccctg  
 30 caaatctagatgtaagcgccaacctctgcactgcctgtggtggggcgcccttcttgacttctcgctggaggtg  
 caggctgcccgtgcccgtctgccagccgggtgaagtgtggcagtcggggccagctccaggccctcagcatcttt  
 gcacaggacctgcgcctctgcctggatgaggccctctcctgggactgtttcgccctctcgctgctggctgtggct  
 ctgggcctgggtgtgcccctgctgcacacctctgtggtgggacctctggtactgcttccacctgtgctggcc  
 tggcttccctggcggggggcggaagtggggcgagatgaggatgcccctgcctacgatgccttctggttcttcgac  
 35 aaaacgcagagcgcagtggtgagactgggtgtacaacgagcttcggggggcagctggaggagtgcctggggcgctgg  
 gcaactccgctgtgctggaggaaacgcgactggctgcctggcaaaacctctttgagaacctgtgggcctcggtc  
 tatggcagccgcaagacgctgtttgtgctggccacacagcgggtcagtggtctcttgccgcccagcttctcgt  
 ctggcccagcagccgctgtgaggaccgcaaggacgtcgtggtgctggtgatcctgagccctgacggccgcccgc  
 tcccgtacgtgcccgtgcgccagcgcctctgcgcagagtgctcctcctctggccccaccagcccagtggtcag  
 40 cgcagcttctggggccagctgggcatggccctgaccagggaacaccacttctataaccggaacttctgcccag  
 ggacccacggccgaatagccgtgagccggaatcctgcacggtgccacctccacactcacctcacctctgcctgcc  
 tggctgacccctcccctgctgcctccctcaccacacacctgacacagagca

## SEQ ID NO:36 (Human TLR9)

atgggtttctgccgcagcgccttgcaaccgctgtctctcctgggtgcaggccatcatgctggccatgaccctggcc  
 ctgggtaccttgccctgccttctaccctgtgagctccagccccacggcctggtgaactgcaactggctgttctctg  
 aagtctgtgccccacttctccatggcagcaccctgtggcaatgtcaccagcctttccttgctcctccaaccgcatc  
 caccacctccatgattctgactttgcccacctgcccagctgcggcatctcaacctcaagtggaaactgcccgcg  
 gttggcctcagccccatgcacttcccctgccacatgaccatcgagcccagcacttcttggtgtgcccaccctg  
 50 gaagagctaaacctgagctacaacaacatcatgactgtgcctgcgctgcccacaaatccctcatatccctgtccctc  
 agccataaccaatcctgatgctagactctgcccagcctgcgcggcctgcatgcccctgcgcttctattcatggac  
 ggcaactgttattacaagaacccctgcaggcaggcactggaggtggccccgggtgcccctccttgccctgggcaac  
 ctacccacctgtcactcaagtacaacaacctcactgtggtgccccgcaacctgccttccagcctggagtatctg  
 ctgttgcctacaaccgcatcgtcaaacctggcgctgaggacctggccaatctgaccgcccctgcgtgtgctcgat  
 55 gtgggggaaattgcccgcgctgcgaccagctcccaacccctgcatggagtgcctcgtcacttccccagcta  
 catcccagctaccttcagccacctgagccgtcttgaaggcctgggtgttgaaggacagttctctctcctggctgaat  
 gccagttgggtccgtgggctgggaaacctccgagtgctggacctgagtgagaacttctctacaaatgcatcact

- 28 -

aaaaccaaggccttccagggcctaacacagctgcgcaagcttaacctgtccttcaattaccaaagagggtgtcc  
 ttgtccacacctgtctctggcccttcttctcgaggagcctggctcgccctgaaggagctggacatgcacggcatcttc  
 tccgctcactcgatgagaccagctccggccactggccgcctgccatgctccagactctgcgtctgcagatg  
 aacttcatcaaccaggcccagctcggcatcttcagggccttccctggcctgcgctacgtggacctgtcggacaac  
 5 cgcatcagcggagcttcggagctgacagccaccatgggggaggcagatggaggggagaaggtctggctgcagcct  
 ggggaccttgctcggcccccagtggaactcccagctctgaagacttcaggcccaactgcagcaccctcaacttc  
 accttggatctgtcacggaacaacctggtgacctgcagccggagatgtttgccagctctcgcacctgcagtgc  
 ctgcgctgagccacaactgcatctcgcaggcagtcattggctcccagttcctgccgctgaccggtctgcagggtg  
 ctagacctgtcccgaataagctggacctctaccacgagcactcattcacggagctaccgcgactggaggccctg  
 10 gacctcagctacacagccagcccttggcatgcaggcgctggggccacaacttcagcttctgggtcacctgcgc  
 accctgcgccacctcagcctggcccaacaacatccacagccaagtgtcccagcagctctgcagtagctcgctg  
 cgggacctggacttcagcggcaatgcactgggccatatgtgggcccaggagacctctatctgcacttcttccaa  
 ggctgagcgggttgatctggctggacttgtcccagaaccgcctgcacaccctcctgcccacaacctgcgcaac  
 ctccccaaagagcctacaggtgctgcgtctccgtgacaattacctggccttctttaagtgtggagcctccacttc  
 15 ctgcccacaactggaagtctcgcacctggcaggaaccggctgaaggccctgaccaatggcagcctgctgctggc  
 accggctccggaggtggtgctcagctgcaacagcatcagcttcgtggccccggcttcttttccaaggccaag  
 gagctgcgagagctcaaccttagcgccaacgcctcaagacagtggaactcctgggttggggccctgcgagtg  
 gccctgcaatactagatgtaagcgccaacctctgcactgcgcctgtggggcgccctttaggacttctgctg  
 gaggtgcaggctgccgtgccggcttgcagccgggtgaagtgtggcagtcggggccagctccagggcctcagc  
 20 atctttgcacaggacctgcgcctctgcctggatgaggccctctcctgggactgtttcgcc

In addition to the foregoing native rat, porcine, bovine, equine, and ovine TLR9  
 polypeptides and nucleic acid molecules encoding them, chimeric TLR9 polypeptides and  
 nucleic acid molecules encoding them are provided by the invention. The chimeric  
 25 polypeptides include at least one amino acid substitution based on a comparison of  
 conserved and non-conserved amino acids among at least two of rat, murine, porcine, bovine,  
 equine, ovine, canine, feline, and human TLR9. The information contained in a multiple  
 sequence alignment of these various TLR9 polypeptide sequences, provided for example in  
 Figure 1, can be used to identify and select individual amino acid positions and even  
 30 individual amino acids to substitute in designing a chimeric TLR9. The substitution or  
 substitutions can be effected using methods known to those of ordinary skill in molecular  
 biology. Nucleic acids encoding the native or chimeric polypeptides of the invention can be  
 inserted into an expression vector and used to express TLR9 polypeptide.

A conservative amino acid substitution shall refer to a substitution of a first amino  
 35 acid for a second amino acid, wherein side chains of the first amino acid and the second  
 amino acid share similar features in terms of hydrophobicity, size, aromaticity, or tendency to  
 alter conformation. For example, conservative amino acid substitutions generally may be  
 made between members within each of the following groups: hydrophobic (A, I, L, M, V),  
 neutral (C, S, T), acidic (D, E), basic (H, K, N, Q, R), and aromatic (F, W, Y). A non-  
 40 conservative amino acid substitution refers to any other amino acid substitution.

- 29 -

An expression vector for TLR9 will include at least a nucleotide sequence coding for a TLR9, or a fragment thereof coding for a functional TLR9 polypeptide, operably linked to a gene expression sequence which can direct the expression of the TLR9 nucleic acid within a eukaryotic or prokaryotic cell. A "gene expression sequence" is any regulatory nucleotide  
5 sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the nucleic acid to which it is operably linked. With respect to TLR9 nucleic acid, the "gene expression sequence" is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the TLR9 nucleic acid to which it is  
10 operably linked. The gene expression sequence may, for example, be a mammalian or viral promoter, such as a constitutive or inducible promoter. Constitutive mammalian promoters include, but are not limited to, the promoters for the following genes: hypoxanthine phosphoribosyl transferase (HPRT), adenosine deaminase, pyruvate kinase,  $\beta$ -actin promoter, and other constitutive promoters. Exemplary viral promoters which function constitutively in  
15 eukaryotic cells include, for example, promoters from the simian virus (e.g., SV40), papillomavirus, adenovirus, human immunodeficiency virus (HIV), Rous sarcoma virus (RSV), cytomegalovirus (CMV), the long terminal repeats (LTR) of Moloney murine leukemia virus and other retroviruses, and the thymidine kinase (TK) promoter of herpes simplex virus. Other constitutive promoters are known to those of ordinary skill in the art.  
20 The promoters useful as gene expression sequences of the invention also include inducible promoters. Inducible promoters are expressed in the presence of an inducing agent. For example, the metallothionein (MT) promoter is induced to promote transcription and translation in the presence of certain metal ions. Other inducible promoters are known to those of ordinary skill in the art.

25 In general, the gene expression sequence shall include, as necessary, 5' non-transcribing and 5' non-translating sequences involved with the initiation of transcription and translation, respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribing sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined nucleic acid  
30 coding sequence for a TLR9 polypeptide. The gene expression sequences optionally include enhancer sequences or upstream activator sequences as desired.

- 30 -

Generally a nucleic acid coding sequence and a gene expression sequence are said to be “operably linked” when they are covalently linked in such a way as to place the transcription and/or translation of the nucleic acid coding sequence under the influence or control of the gene expression sequence. Thus the TLR9 nucleic acid coding sequence and the gene expression sequence are said to be “operably linked” when they are covalently linked in such a way as to place the transcription and/or translation of the TLR9 nucleic acid coding sequence under the influence or control of the gene expression sequence. If it is desired that the TLR9 sequence be translated into a functional protein, two DNA sequences are said to be operably linked if induction of a promoter in the 5' gene expression sequence results in the transcription of the TLR9 sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the TLR9 sequence, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a gene expression sequence would be operably linked to a TLR9 nucleic acid sequence if the gene expression sequence were capable of effecting transcription of that TLR9 nucleic acid sequence such that the resulting transcript might be translated into the desired TLR9 protein or polypeptide.

A “TLR9 ligand” as used herein refers to a molecule that specifically binds a TLR9 polypeptide. In one embodiment the TLR9 ligand specifically binds a TLR9 polypeptide corresponding to at least a ligand-binding portion of the extracellular domain of TLR9. In most instances a TLR9 ligand will also induce TLR9 signaling when contacted with TLR9 under suitable conditions. TLR9 signaling refers to TLR/IL-1R signal transduction mediated through the TLR9, as described in further detail elsewhere herein. As mentioned above, CpG nucleic acids have been reported to be TLR9 ligands, but TLR9 ligands may include other entities as well, including, for example, small molecules. As also previously mentioned, there appears to be a species-specific preference for at least certain TLR9s and certain CpG motifs. As used herein, a species-preferred CpG DNA refers to a particular CpG DNA that is optimized for signal induction by a TLR9 of a particular species. A CpG DNA that is optimized for signal induction by a TLR9 of a particular species refers to a CpG DNA having a sequence that preferentially binds to and/or induces signaling by TLR9 of that species. For example, a human-preferred CpG DNA shall refer to a CpG DNA that optimally stimulates human TLR9 to signal through its TIR domain. Likewise, a murine-preferred CpG DNA

- 31 -

shall refer to a CpG DNA that optimally stimulates murine TLR9 to signal through its TIR domain. Examples of human-preferred and murine-preferred CpG DNA are ODN 2006 (SEQ ID NO:58) and 1668 (SEQ ID NO:60), respectively.

5 The binding and species specificity of TLR9s are believed to be influenced by key amino acids present in the extracellular domain of TLR9. Key amino acids in a TLR9 as used herein refer to those amino acids which contribute significantly to ligand binding and ligand specificity of a particular TLR9 polypeptide.

A "CpG nucleic acid" or a "CpG immunostimulatory nucleic acid" as used herein is a nucleic acid containing at least one unmethylated CpG dinucleotide (cytosine-guanine  
10 dinucleotide sequence, i.e., "CpG DNA" or DNA containing a 5' cytosine followed by 3' guanine and linked by a phosphate bond) which activates a component of the immune system. The entire CpG nucleic acid can be unmethylated or portions may be unmethylated but at least the C of the 5' CG 3' must be unmethylated.

In one embodiment a CpG nucleic acid is represented by at least the formula:

15 
$$5'-N_1X_1CGX_2N_2-3'$$

wherein  $X_1$  and  $X_2$  are nucleotides, N is any nucleotide, and  $N_1$  and  $N_2$  are nucleic acid sequences composed of from about 0-25 N's each. In some embodiments  $X_1$  is adenine, guanine, or thymine and/or  $X_2$  is cytosine, adenine, or thymine. In other embodiments  $X_1$  is cytosine and/or  $X_2$  is guanine.

20 Nucleic acids having modified backbones, such as phosphorothioate backbones, also fall within the class of immunostimulatory nucleic acids. U.S. Pat. Nos. 5,723,335 and 5,663,153 issued to Hutcherson, et al. and related PCT publication WO95/26204 describe immune stimulation using phosphorothioate oligonucleotide analogues. These patents describe the ability of the phosphorothioate backbone to stimulate an immune response in a  
25 non-sequence specific manner.

An immunostimulatory nucleic acid molecule, including for example a CpG DNA, may be double-stranded or single-stranded. Generally, double-stranded molecules may be more stable *in vivo*, while single-stranded molecules may have increased activity. The terms "nucleic acid" and "oligonucleotide" refer to multiple nucleotides (i.e., molecules comprising  
30 a sugar (e.g., ribose or deoxyribose) linked to a phosphate group and to an exchangeable organic base, which is either a substituted pyrimidine (e.g., cytosine (C), thymine (T) or uracil (U)) or a substituted purine (e.g., adenine (A) or guanine (G)) or a modified base. As

- 32 -

used herein, the terms "nucleic acid" and "oligonucleotide" refer to oligoribonucleotides as well as oligodeoxyribonucleotides. The terms shall also include polynucleosides (i.e., a polynucleotide minus the phosphate) and any other organic base-containing polymer. The terms "nucleic acid" and "oligonucleotide" also encompass nucleic acids or oligonucleotides  
5 with a covalently modified base and/or sugar. For example, they include nucleic acids having backbone sugars which are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 2' position and other than a phosphate group at the 5' position. Thus modified nucleic acids may include a 2'-O-alkylated ribose group. In addition, modified nucleic acids may include sugars such as arabinose instead of ribose. Thus the  
10 nucleic acids may be heterogeneous in backbone composition thereby containing any possible combination of polymer units linked together such as peptide-nucleic acids (which have amino acid backbone with nucleic acid bases). In some embodiments the nucleic acids are homogeneous in backbone composition.

The substituted purines and pyrimidines of the immunostimulatory nucleic acids  
15 include standard purines and pyrimidines such as cytosine as well as base analogs such as C-5 propyne substituted bases. Wagner RW et al. (1996) *Nat Biotechnol* 14:840-4. Purines and pyrimidines include but are not limited to adenine, cytosine, guanine, thymine, 5-methylcytosine, 2-aminopurine, 2-amino-6-chloropurine, 2,6-diaminopurine, hypoxanthine, and other naturally and non-naturally occurring nucleobases, substituted and unsubstituted  
20 aromatic moieties.

The immunostimulatory nucleic acid is a linked polymer of bases or nucleotides. As used herein with respect to linked units of a nucleic acid, "linked" or "linkage" means two entities are bound to one another by any physicochemical means. Any linkage known to those of ordinary skill in the art, covalent or non-covalent, is embraced. Such linkages are  
25 well known to those of ordinary skill in the art. Natural linkages, which are those ordinarily found in nature connecting the individual units of a nucleic acid, are most common. The individual units of a nucleic acid may be linked, however, by synthetic or modified linkages.

Whenever a nucleic acid is represented by a sequence of letters it will be understood that the nucleotides are in 5' to 3' (or equivalent) order from left to right and that "A" denotes adenine, "C" denotes cytosine, "G" denotes guanine, "T" denotes thymidine, and "U" denotes uracil unless otherwise noted.  
30

- 33 -

Immunostimulatory nucleic acid molecules useful according to the invention can be obtained from natural nucleic acid sources (e.g., genomic nuclear or mitochondrial DNA or cDNA), or are synthetic (e.g., produced by oligonucleotide synthesis). Nucleic acids isolated from existing nucleic acid sources are referred to herein as native, natural, or isolated nucleic acids. The nucleic acids useful according to the invention may be isolated from any source, including eukaryotic sources, prokaryotic sources, nuclear DNA, mitochondrial DNA, etc. Thus, the term nucleic acid encompasses both synthetic and isolated nucleic acids.

The immunostimulatory nucleic acids can be produced on a large scale in plasmids, (see *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989) and separated into smaller pieces or administered whole. After being administered to a subject the plasmid can be degraded into oligonucleotides. One skilled in the art can purify viral, bacterial, eukaryotic, etc. nucleic acids using standard techniques, such as those employing restriction enzymes, exonucleases or endonucleases.

For use in the instant invention, the immunostimulatory nucleic acids can be synthesized *de novo* using any of a number of procedures well known in the art. For example, the  $\beta$ -cyanoethyl phosphoramidite method (Beaucage SL and Caruthers MH, *Tetrahedron Let* 22:1859 (1981)); nucleoside H-phosphonate method (Garegg et al., *Tetrahedron Let* 27:4051-4054 (1986); Froehler et al., *Nucl Acid Res* 14:5399-5407 (1986); Garegg et al., *Tetrahedron Let* 27:4055-4058 (1986); Gaffney et al., *Tetrahedron Let* 29:2619-2622 (1988)). These chemistries can be performed by a variety of automated oligonucleotide synthesizers available in the market.

The immunostimulatory nucleic acid may be any size of at least 6 nucleotides but in some embodiments are in the range of between 6 and 100 or in some embodiments between 8 and 35 nucleotides in size. Immunostimulatory nucleic acids can be produced on a large scale in plasmids. These may be administered in plasmid form or alternatively they can be degraded into oligonucleotides before administration.

A "stabilized immunostimulatory nucleic acid" shall mean a nucleic acid molecule that is relatively resistant to *in vivo* degradation (e.g., via an exo- or endo-nuclease).

Stabilization can be a function of length or secondary structure. Nucleic acids that are tens to hundreds of kbs long are relatively resistant to *in vivo* degradation. For shorter nucleic acids, secondary structure can stabilize and increase their effect. For example, if the 3' end of an

- 34 -

oligonucleotide has self-complementarity to an upstream region, so that it can fold back and form a sort of stem loop structure, then the oligonucleotide becomes stabilized and therefore exhibits more activity.

Some stabilized immunostimulatory nucleic acids have a modified backbone. It has  
5 been demonstrated that modification of the oligonucleotide backbone provides enhanced activity of the immunostimulatory nucleic acids when administered *in vivo*. Nucleic acids, including at least two phosphorothioate linkages at the 5' end of the oligonucleotide and multiple phosphorothioate linkages at the 3' end, preferably 5, may provide maximal activity and protect the oligonucleotide from degradation by intracellular exo- and endo-nucleases.  
10 Other modified oligonucleotides include phosphodiester modified oligonucleotide, combinations of phosphodiester and phosphorothioate oligonucleotide, methylphosphonate, methylphosphorothioate, phosphorodithioate, and combinations thereof. Each of these combinations and their particular effects on immune cells is discussed in more detail in U.S. Pat. Nos. 6,194,388 and 6,207,646, the entire contents of which are incorporated herein by  
15 reference. It is believed that these modified oligonucleotides may show more stimulatory activity due to enhanced nuclease resistance, increased cellular uptake, increased protein binding, and/or altered intracellular localization. Both phosphorothioate and phosphodiester nucleic acids are active in immune cells.

Other stabilized immunostimulatory nucleic acids include: nonionic DNA analogs,  
20 such as alkyl- and aryl-phosphates (in which the charged phosphonate oxygen is replaced by an alkyl or aryl group), phosphodiester and alkylphosphotriesters, in which the charged oxygen moiety is alkylated. Oligonucleotides which contain diol, such as tetraethyleneglycol or hexaethyleneglycol, at either or both termini have also been shown to be substantially resistant to nuclease degradation.

25 Phosphorothioate nucleic acid molecules may be synthesized using automated techniques employing either phosphoramidate or H-phosphonate chemistries. Aryl- and alkyl-phosphonates can be made, e.g., as described in U.S. Pat. No. 4,469,863; and alkylphosphotriesters (in which the charged oxygen moiety is alkylated as described in U.S. Pat. No. 5,023,243 and European Patent No. 092,574) can be prepared by automated solid  
30 phase synthesis using commercially available reagents. Methods for making other DNA backbone modifications and substitutions have been described. Uhlmann E and Peyman A (1990) *Chem Rev* 90:544; Goodchild J (1990) *Bioconjugate Chem* 1:165.



- 35 -

Other sources of immunostimulatory nucleic acids useful according to the invention include standard viral and bacterial vectors, many of which are commercially available. In its broadest sense, a "vector" is any nucleic acid material which is ordinarily used to deliver and facilitate the transfer of nucleic acids to cells. The vector as used herein may be an empty  
 5 vector or a vector carrying a gene which can be expressed. In the case when the vector is carrying a gene the vector generally transports the gene to the target cells with reduced degradation relative to the extent of degradation that would result in the absence of the vector. In this case the vector optionally includes gene expression sequences to enhance expression of the gene in target cells such as immune cells, but it is not required that the gene  
 10 be expressed in the cell.

Nucleic acid-binding fragments of TLRs are believed to include the extracytoplasmic (extracellular) domain or subportions thereof, such as those which include at least an MBD motif, a CXXC motif, or both an MBD motif and a CXXC motif.

Both mouse and human TLR9 have an N-terminal extension of approximately 180  
 15 amino acids compared to other TLRs. An insertion also occurs at amino acids 253-268, which is not found in TLRs 1-6 but is present in human TLR7 and human TLR8. This insert has two CXXC motifs which participate in forming a CXXC domain. The CXXC domain resembles a zinc finger motif and is found in DNA-binding proteins and in certain specific CpG binding proteins, e.g., methyl-CpG binding protein-1 (MBD-1). Fujita N et al. (2000)  
 20 *Mol Cell Biol* 20:5107-18. Both human and mouse TLR9 CXXC domains occur at aa 253-268:

CXXC motif:	GNCXXCXXXXXXCXXC	SEQ ID NO:62
Human TLR9:	GNCRRCDHAPNPCMEC	SEQ ID NO:63
25 Murine TLR9:	GNCRRCDHAPNPCMIC	SEQ ID NO:64

An additional motif believed to be involved in CpG binding is the MBD motif, also found in MBD-1, listed below as SEQ ID NO:53. Fujita, N et al.(2000) *Mol Cell Biol* 20:5107-18; Ohki I et al. (1999) *EMBO J* 18:6653-61. Amino acids 524-554 of hTLR9 and  
 30 aa 525-555 of mTLR9 correspond to the MBD motif of MBD-1 as shown:

MBD motif:

- 36 -

	MBD-1	R-XXXXXXXX-R-X-D-X-Y-XXXXXXXXXX-R-S-XXXXXX-Y	SEQ ID NO:65
	hTLR9	Q-XXXXXXXX-K-X-D-X-Y-XXXXXXXXXX-R-L-XXXXXX-Y	SEQ ID NO:66
	mTLR9	Q-XXXXXXXX-K-X-D-X-Y-XXXXXXXXXX-Q-L-XXXXXX-Y	SEQ ID NO:67
5	hTLR9	Q-VLDLSRN-K-L-D-L-Y-HEHSFTELP-R-L-EALDLS-Y	SEQ ID NO:68
	mTLR9	Q-VLDLSHN-K-L-D-L-Y-HWKSFSERP-Q-L-QALDLS-Y	SEQ ID NO:69

Although the signaling functions of MBD-1 and TLR9 are quite different, the core D-X-Y is conserved and is believed to be involved in CpG binding.

10 According to another aspect of the invention, a screening method is provided for identifying an immunostimulatory compound. The method according to this aspect of the invention involves contacting a functional TLR9 with a test compound; detecting presence or absence of a response mediated by a TLR9 signal transduction pathway in the presence of the test compound arising as a result of an interaction between the functional TLR9 and the test  
15 compound; and determining the test compound is an immunostimulatory compound when the presence of a response mediated by the TLR9 signal transduction pathway is detected.

An immunostimulatory compound is a natural or synthetic compound that is capable of inducing an immune response when contacted with an immune cell. A TLR9 ligand that is an immunostimulatory compound is a natural or synthetic compound that is capable of  
20 inducing an immune response when contacted with an immune cell that expresses TLR9. A TLR9 ligand that is an immunostimulatory compound is also a natural or synthetic compound that is capable of inducing a TLR/IL-1R signal transduction pathway when contacted with a TLR9. Immunostimulatory compounds include but are not limited to immunostimulatory  
25 nucleic acids. The immunostimulatory compound can be, for example, a nucleic acid molecule, polynucleotide or oligonucleotide, a polypeptide or oligopeptide, a lipid or lipopolysaccharide, a small molecule.

A basis for certain of the screening assays is the presence of a functional TLR9 in a cell. The functional TLR9 in some instances is naturally expressed by a cell. In other instances, expression of the functional TLR9 can involve introduction or reconstitution of a  
30 species-specific TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact with an

- 37 -

immunostimulatory nucleic acid. In yet other instances, expression of the functional TLR9 can involve introduction of a chimeric or modified TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact  
5 with an immunostimulatory nucleic acid. Examples of cell lines lacking TLR9 or immunostimulatory nucleic acid responsiveness include, but are not limited to, 293 fibroblasts (ATCC CRL-1573), MonoMac-6, THP-1, U937, CHO, and any TLR9 knock-out. The introduction of the species-specific, chimeric or modified TLR9 into the cell or cell line is preferably accomplished by transient or stable transfection of the cell or cell line with a  
10 TLR9-encoding nucleic acid sequence operatively linked to a gene expression sequence (as described above). Methods for transient and for stable transfection of a cell are well known in the art.

The screening assays can have any of a number of possible readout systems based upon either TLR/IL-1R signaling pathway or other assays useful for assessing response to  
15 immunostimulatory nucleic acids. It has been reported that immune cell activation by CpG immunostimulatory sequences is dependent in some way on endosomal processing.

In certain embodiments, the readout for the screening assay is based on the use of native genes or, alternatively, cotransfected or otherwise co-introduced reporter gene constructs which are responsive to the TLR/IL-1R signal transduction pathway involving  
20 MyD88, TRAF, p38, and/or ERK. Häcker H et al. (1999) *EMBO J* 18:6973-6982. These pathways activate kinases including  $\kappa$ B kinase complex and c-Jun N-terminal kinases. Thus reporter genes and reporter gene constructs particularly useful for the assays can include a reporter gene operatively linked to a promoter sensitive to NF- $\kappa$ B. Examples of such promoters include, without limitation, those for NF- $\kappa$ B, IL-1 $\beta$ , IL-6, IL-8, IL-12 p40, CD80,  
25 CD86, and TNF- $\alpha$ . The reporter gene operatively linked to the TLR-sensitive promoter can include, without limitation, an enzyme (e.g., luciferase, alkaline phosphatase,  $\beta$ -galactosidase, chloramphenicol acetyltransferase (CAT), etc.), a bioluminescence marker (e.g., green-fluorescent protein (GFP, U.S. Pat. No. 5,491,084), blue fluorescent protein, etc.), a surface-expressed molecule (e.g., CD25), and a secreted molecule (e.g., IL-8, IL-12 p40, TNF- $\alpha$ ). In  
30 certain embodiments the reporter is selected from IL-8, TNF- $\alpha$ , NF- $\kappa$ B-luciferase (NF- $\kappa$ B-luc; Häcker H et al. (1999) *EMBO J* 18:6973-6982), IL-12 p40-luc (Murphy TL et al. (1995)

- 38 -

*Mol Cell Biol* 15:5258-5267), and TNF-luc (Häcker H et al. (1999) *EMBO J* 18:6973-6982). At least one of these reporter constructs (NF- $\kappa$ B-luc) is commercially available (Stratagene, La Jolla, CA). In assays relying on enzyme activity readout, substrate can be supplied as part of the assay, and detection can involve measurement of chemiluminescence, fluorescence, color development, incorporation of radioactive label, drug resistance, or other marker of enzyme activity. For assays relying on surface expression of a molecule, detection can be accomplished using FACS analysis or functional assays. Secreted molecules can be assayed using enzyme-linked immunosorbent assay (ELISA) or bioassays. Many such readout systems are well known in the art and are commercially available.

10 According to one embodiment of this method, comparison can be made to a reference immunostimulatory nucleic acid. The reference immunostimulatory nucleic acid may be any suitably selected immunostimulatory nucleic acid, including a CpG nucleic acid. In certain embodiments the screening method is performed using a plurality of test nucleic acids. In certain embodiments comparison of test and reference responses is based on comparison of quantitative measurements of responses in each instance.

15 In another aspect the invention provides a screening method for identifying species specificity of an immunostimulatory nucleic acid. The method involves contacting a TLR9 of a first species with a test immunostimulatory nucleic acid; contacting a TLR9 of a second species with the test immunostimulatory nucleic acid; measuring a response mediated by a TLR signal transduction pathway associated with the contacting the TLR9 of the first species with the test immunostimulatory nucleic acid; measuring a response mediated by the TLR signal transduction pathway associated with the contacting the TLR9 of the second species with the test immunostimulatory nucleic acid; and comparing the two responses. The TLR9 may be expressed by a cell or it may be part of a cell-free system. The TLR9 may be part of a complex, with either another TLR or with another protein, e.g., MyD88, IRAK, TRAF, I $\kappa$ B, NF- $\kappa$ B, or functional homologues and derivatives thereof. Thus for example a given ODN can be tested against a panel of human fibroblast 293 fibroblast cells transfected with TLR9 from various species and optionally cotransfected with a reporter construct sensitive to TLR/IL-1R activation pathways. Thus in another aspect, the invention provides a method for screening species selectivity with respect to a given nucleic acid sequence.

30 Test compounds can include but are not limited to peptide nucleic acids (PNAs), antibodies, polypeptides, carbohydrates, lipids, hormones, and small molecules. Test

- 39 -

compounds can further include variants of a reference immunostimulatory nucleic acid incorporating any one or combination of the substitutions described above. Test compounds can be generated as members of a combinatorial library of compounds.

In preferred embodiments, the screening methods can be performed on a large scale and with high throughput by incorporating, e.g., an array-based assay system and at least one automated or semi-automated step. For example, the assays can be set up using multiple-well plates in which cells are dispensed in individual wells and reagents are added in a systematic manner using a multiwell delivery device suited to the geometry of the multiwell plate. Manual and robotic multiwell delivery devices suitable for use in a high throughput screening assay are well known by those skilled in the art. Each well or array element can be mapped in a one-to-one manner to a particular test condition, such as the test compound. Readouts can also be performed in this multiwell array, preferably using a multiwell plate reader device or the like. Examples of such devices are well known in the art and are available through commercial sources. Sample and reagent handling can be automated to further enhance the throughput capacity of the screening assay, such that dozens, hundreds, thousands, or even millions of parallel assays can be performed in a day or in a week. Fully robotic systems are known in the art for applications such as generation and analysis of combinatorial libraries of synthetic compounds. See, for example, U.S. Pat. Nos. 5,443,791 and 5,708,158.

The following examples are provided for illustrative purposes and are not meant to be limiting in any way.

### Examples

Example 1. Cloning and Sequencing of Rat, Porcine, Bovine, Equine, Ovine, Canine, and Feline TLR9

*Cells and Tissues.* Lymphoid tissues, primarily spleen or blood mononuclear cells (PBMC) from five mammalian species were collected: mouse, pig, bovine, rat and horse. Spleen samples were collected in RNeasy<sup>TM</sup> (Ambion<sup>®</sup>, Austin, TX, USA), stabilized at 4°C overnight and stored at -70°C. Blood samples were centrifuged at 500 x g for 25 min at room temperature and the buffy coat, containing enriched PBMC, was then removed and stored at -70°C. The mouse specimen was used as a comparative positive control.

- 40 -

*First-strand cDNA synthesis.* Total RNA from the spleen and PBMC samples was isolated using a monophasic solution of phenol and guanidine isothiocyanate: TRIzol™ reagent (GIBCO BRL®, Burlington, ON, Canada) according to the manufacturer's instructions. First-strand cDNA was synthesized from the total RNA using  
5 SUPERScript™ II reverse transcriptase (GIBCO BRL®, Burlington, ON, Canada). Approximately 3 µg of total RNA was added to 50 pmoles of oligo(dT) primer [poly T<sub>(18)</sub>]; the mixture was heated to 70°C for 10 min and subsequently chilled on ice. The following was added to the cooled reaction mixture: 1 µl of mixed dNTP stock containing 10 mM each dATP, dCTP, dGTP and dTTP (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) at  
10 neutral pH, 1X first strand buffer (50 mM Tris-HCl pH 8.3/ 75 mM KCl/ 3 mM MgCl<sub>2</sub>) and 2 µl of 0.1 M DTT. The mixture was subsequently heated to 42°C for 2 min, followed by addition of 200 units of SUPERScript™ II reverse transcriptase. The reaction was carried out at 42°C for 50 min, followed by 70°C for 15 min. The first-strand cDNA was used as the template for subsequent polymerase chain reaction (PCR) amplifications.

15 *PCR amplification.* TLR9 gene was PCR amplified from each of the above-mentioned species using primers designed from known mouse and human TLR9 sequence in Genbank: Accession AF314224 and AF259262, respectively. The primers were designed using the primer design software, Clone Manager 5 (Scientific and Educational Software, Durham, NC, USA). TLR9 gene-specific primers used were:  
20 forward primer 5'-ACCTTGCCTGCCTTCCTACCCTGTGA-3' (SEQ ID NO:37) and reverse primer 5'-GTCCGTGTGGGCCAGCACAAA-3' (SEQ ID NO:38).

The 2.7 Kbp fragment was PCR amplified using Advantage® 2 DNA polymerase mix (BD Biosciences Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. PCR reaction volumes of 25 µl contained 15 pmoles of each primer, 0.2 mM of dNTP mix  
25 and 1 µl of reverse transcription reaction. PCR amplification was conducted by initial denaturation at 94°C for 1 min followed by 30 cycles of 94°C denaturation (15 sec), 65°C annealing (45 sec) and 72°C extensions (2 min), with a final extension at 72°C for 5 min.

*Cloning and sequencing.* The PCR amplified fragment was treated with 500 units of T4 DNA polymerase (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) for 15 min  
30 at room temperature prior to cleaning the reaction with QIAquick PCR purification kit (QIAGEN Inc., Mississauga, ON, Canada). The fragment was then ligated to pZerO™ - 2

- 41 -

vector (Invitrogen™ Life Technologies, Burlington, ON, Canada), treated with *Eco RV* restriction enzyme, using T4 DNA Ligase (GIBCO BRL®, Burlington, ON, Canada). *E. coli* TOP 10 chemically competent cells (Invitrogen™ Life Technologies, Burlington, ON, Canada) were used to transform ligated products. Plasmids containing the 2.7 Kbp fragment were sequenced using an automated DNA sequencer, CEQ™ 2000XL DNA analysis system (Beckman Coulter Inc., Fullerton, CA, USA).

Sequences of the 2.7 Kbp fragment were derived from three clones of each species selected from independent PCR reactions to account for errors that may have been incurred during the PCR amplifications and to confirm the sequence data.

Nucleotide sequences of the rat, porcine, bovine, equine, ovine, canine, and feline TLR9 were extended and completed using standard 5' and 3' RACE PCR and primers designed using the sequences obtained from the 2.7 Kbp fragments.

**Results.** Nucleotide sequences of rat, porcine, bovine, equine, canine, and feline TLR9 cDNA obtained by the methods above are provided as SEQ ID NOs 3, 7, 11, 15, 19, 23, and 27, respectively. Deduced amino acid sequences are provided as SEQ ID NOs 1, 5, 9, 13, 17, 21, and 25, respectively. Deduced amino acid sequences of full-length murine and human TLR9 are provided as SEQ ID NOs 29 and 33, respectively.

#### Example 2. Comparison of Aligned Sequences for TLR9 from Various Mammalian Species.

Multiple sequence alignment of deduced amino acid sequences for feline, canine, bovine, mouse, ovine, porcine, horse, human, and rat TLR9 polypeptides was performed using Clustal W 1.82 (see, for example, [www.cmbi.kun.nl/bioinf/tools/clustalw.shtml](http://www.cmbi.kun.nl/bioinf/tools/clustalw.shtml)). In addition, paired sequence alignment of deduced amino acid sequences for murine and human TLR9 polypeptides was performed using Clustal W 1.82. The results of the multiple sequence alignment are presented in **Figure 1**. As will be appreciated from Figure 1, certain amino acids are highly conserved across all species examined. Similarly, certain amino acids differ only by conservative amino acid substitutions among the various species. In addition, it is evident that certain amino acids which are conserved between murine and human TLR9 are not conserved in other species. Furthermore, Figure 1 also indicates that certain amino acids are highly divergent across various species. The information provided by the comparison of multiple species adds significantly to the information available by comparison between only murine and human TLR9 sequences.

- 42 -

The putative transmembrane regions of the TLR9 polypeptides are indicated in boxes in Figure 1. Sequence upstream of each transmembrane region is extracellular domain and is believed to include sequence primarily responsible for binding to TLR9 ligands, including CpG DNA. The extracellular domains of feline, canine, bovine, mouse, ovine, porcine, horse, human, and rat TLR9 correspond to amino acids numbered 1-820, 1-822, 1-818, 1-821, 1-818, 1-819, 1-820, 1-820, and 1-821, respectively, as shown in Figure 1.

**Figure 2** presents an evolutionary relatedness tree for six TLR9 polypeptides examined. The cladogram in Figure 2 was prepared using Clustal W (see above). As can be appreciated from this figure, murine and human TLR9 are nearly the most divergent TLR9s in this group. Surprisingly, human and horse TLR9 appear relatively closely related.

### Example 3. Reconstitution of TLR9 Signaling in 293 Fibroblasts.

Mouse TLR9 cDNA (SEQ ID NO:31) and human TLR9 cDNA (SEQ ID NO:35) in pT-Adv vector (from Clontech) were individually cloned into the expression vector pcDNA3.1(-) from Invitrogen using the EcoRI site. Utilizing a "gain of function" assay it was possible to reconstitute human TLR9 (hTLR9) and murine TLR9 (mTLR9) signaling in CpG-DNA non-responsive human 293 fibroblasts (ATCC, CRL-1573). The expression vectors mentioned above were transfected into 293 fibroblast cells using the calcium phosphate method.

Since NF- $\kappa$ B activation is central to the IL-1/TLR signal transduction pathway (Medzhitov R et al. (1998) *Mol Cell* 2:253-258; Muzio M et al. (1998) *J Exp Med* 187:2097-101), cells were transfected with hTLR9 or co-transfected with hTLR9 and an NF- $\kappa$ B-driven luciferase reporter construct. Human fibroblast 293 cells were transiently transfected with hTLR9 and a six-times NF- $\kappa$ B-luciferase reporter plasmid (NF- $\kappa$ B-luc) or with hTLR9 alone. After stimulus with CpG-ODN (2006, 2 $\mu$ M, TCGTCGTTTTGTCGTTTTGTCGTT, SEQ ID NO:58), GpC-ODN (2006-GC, 2 $\mu$ M, TGCTGCTTTTGTGCTTTTGTGCTT, SEQ ID NO:59), LPS (100 ng/ml) or media, NF- $\kappa$ B activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results representative of three independent experiments showed that cells expressing hTLR9 responded to CpG-DNA but not to LPS.

Independently, human fibroblast 293 cells were transiently transfected with mTLR9 and the NF- $\kappa$ B-luc construct or with mTLR9 alone. After stimulation with CpG-ODN (1668, 2 $\mu$ M; TCCATGACGTTCTGATGCT, SEQ ID NO:60), GpC-ODN (1668-GC, 2 $\mu$ M;



- 43 -

TCCATGAGCTTCCTGATGCT, SEQ ID NO:61), LPS (100 ng/ml) or media, NF- $\kappa$ B activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results showed that expression of TLR9 (human or mouse) in 293 cells results in a gain of function for CpG-DNA stimulation.

5 To generate stable clones expressing human TLR9, murine TLR9, or either TLR9 with the NF- $\kappa$ B-luc reporter plasmid, 293 cells were transfected in 10 cm plates ( $2 \times 10^6$  cells/plate) with 16  $\mu$ g of DNA and selected with 0.7 mg/ml G418 (PAA Laboratories GmbH, Cölbe, Germany). Clones were tested for TLR9 expression by RT-PCR. The clones were also screened for IL-8 production or NF- $\kappa$ B-luciferase activity after stimulation with  
10 ODN. Four different types of clones were generated.

293-hTLR9-luc:	expressing human TLR9 and 6-fold NF- $\kappa$ B-luciferase reporter
293-mTLR9-luc:	expressing murine TLR9 and 6-fold NF- $\kappa$ B-luciferase reporter
293-hTLR9:	expressing human TLR9
15 293-mTLR9:	expressing murine TLR9

Results indicated that stable clones also responded to CpG-ODN.

Example 4. Similar ODN Sequence Specificity of TLR9 of Human and Equine TLR9.

20  $3 \times 10^6$  293T cells were electroporated with 5  $\mu$ g NF- $\kappa$ B-luc plasmid and 5  $\mu$ g of either horse TLR9-pcDNA3.1 plasmid or humanTLR9-pcDNA3.1 plasmid at 200V, 975  $\mu$ F. After the electroporation the cells were plated in 96-well cell culture plates at  $2.5 \times 10^4$  cells per well and grown overnight at 37°C. The cells were stimulated with the indicated concentration of ODN for 16h, after which the supernatant was removed and the cells lysed in lysis buffer and  
25 frozen for at least 2 hours at -80°C. Luciferase activity was measured by adding Luciferase Assay substrate from Promega. Values are given as fold specific induction over non-stimulated control. Results are shown in Figure 3.

As shown in Figure 3, ODN 2006 (TCGTCGTTTTGTCGTTTTGTCGTT; SEQ ID NO:58) has a strong specificity for human TLR9. ODN 1982  
30 (TCCAGGACTTCTCTCAGGTT; SEQ ID NO:70) was the negative control ODN. ODN 5890 (TCCATGACGTTTTTGATGTT; SEQ ID NO:39) has a strong specificity for mouse

- 44 -

TLR9. This experiment demonstrates the similarity of horse TLR9 to human TLR9 in binding specificity, a result predicted by the evolutionary relatedness of horse TLR9 to human TLR9. Mouse TLR9 is more distant from horse TLR9 and human TLR9 in sequence homology, and ODN 5890 was not detected by either human or horse TLR9.

5

Example 5. Non-human, Non-murine Native Mammalian TLR9 Useful in Screening for Human-Preferred CpG DNA.

Native rat, porcine, bovine, equine, and ovine TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Rat, porcine, bovine, equine, or ovine TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

20 Example 6. Chimeric TLR9 Useful in Screening for Human-Preferred CpG DNA.

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

30

Example 7. Chimeric TLR9 Responsive to Both Human-Preferred and Murine-Preferred CpG DNA.

- 45 -

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006) and also screened for binding or TLR9 signaling activity when contacted with murine-preferred CpG DNA (ODN 1668). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in each of these assays are then used as the basis for screening for additional human-preferred CpG DNA and for screening for additional murine-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA or candidate murine-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA. Candidate murine-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as murine-preferred CpG DNA.

### Equivalents

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by examples provided, since the examples are intended as a single illustration of one aspect of the invention and other functionally equivalent embodiments are within the scope of the invention. Various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims. The advantages of the invention are not necessarily encompassed by each embodiment of the invention.

All references, patents and patent publications that are recited in this application are incorporated in their entirety herein by reference.

We claim:

- 46 -

### Claims

1. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.  
5
2. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.
3. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a  
10 polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.
4. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ  
15 ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.
5. A vector comprising the nucleic acid of any of claims 3-4.
6. A cell comprising the vector of claim 5.  
20
7. An antibody or fragment thereof that binds specifically to the polypeptide of any of claims 1-2.
8. A method for identifying key amino acids in a TLR9 of a first species which  
25 confer specificity for CpG DNA optimized for TLR9 of the first species, comprising:  
aligning protein sequences of TLR9 of a first species, TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species;  
30 generating an initial set of candidate amino acids in the TLR9 of the first species by excluding each amino acid in the TLR9 of the first species which (a) is identical with the

- 47 -

TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

10 9. A method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9, comprising:

aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a CpG DNA optimized for murine TLR9;

generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids.

25

10. The method according to claim 9, performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight, said weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred CpG DNA).

30

- 48 -

11. An isolated polypeptide comprising an amino acid sequence identical to SEQ ID NO:30 except for substitution of at least one key amino acid identified according to the method of any of claims 9 or 10.

5           12. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide according to claim 11.

13. A vector comprising the nucleic acid of claim 12.

10           14. A cell comprising the vector of claim 13.

15. An antibody that binds specifically to the polypeptide of claim 14.

16. A screening method to identify a TLR9 ligand, comprising:  
15           contacting a polypeptide according to any of claims 1, 2, or 11 with a candidate TLR9 ligand;  
              measuring a signal in response to the contacting; and  
              identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling.

20           17. The method of claim 16, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

25           18. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF- $\kappa$ B.

19. The method of claim 17, wherein the candidate TLR9 ligand is an immunostimulatory nucleic acid.

30           20. The method of claim 19, wherein the immunostimulatory nucleic acid is CpG DNA.

- 49 -

21. A screening method to identify species-specific CpG-motif preference of an isolated polypeptide of claim 2 or claim 11, comprising:

contacting an isolated polypeptide of claim 2 or claim 11 with a CpG DNA comprising a hexamer sequence selected from the group consisting of GACGTT, AACGTT, 5 CACGTT, TACGTT, GGCGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG;

measuring a signal in response to the contacting; and

identifying a species-specific CpG-motif preference when the signal in response to the 10 contacting is consistent with TLR9 signaling.

22. The method of claim 21, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

15 23. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF- $\kappa$ B.

24. The method of claim 21, wherein the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

20	TCCATGACGTTTTTGATGTT	(SEQ ID NO:39),
	TCCATAACGTTTTTGATGTT	(SEQ ID NO:40),
	TCCATCACGTTTTTGATGTT	(SEQ ID NO:41),
	TCCATTACGTTTTTGATGTT	(SEQ ID NO:42),
	TCCATGGCGTTTTTGATGTT	(SEQ ID NO:43),
25	TCCATGCCGTTTTTGATGTT	(SEQ ID NO:44),
	TCCATGTCGTTTTTGATGTT	(SEQ ID NO:45),
	TCCATGATGTTTTTGATGTT	(SEQ ID NO:46),
	TCCATGAAGTTTTTGATGTT	(SEQ ID NO:47),
	TCCATGAGGTTTTTGATGTT	(SEQ ID NO:48),
30	TCCATGACATTTTTGATGTT	(SEQ ID NO:49),
	TCCATGACCTTTTTGATGTT	(SEQ ID NO:50),
	TCCATGACTTTTTTGATGTT	(SEQ ID NO:51),
	TCCATGACGCTTTTGATGTT	(SEQ ID NO:52),
	TCCATGACGATTTTGATGTT	(SEQ ID NO:53),
35	TCCATGACGGTTTTGATGTT	(SEQ ID NO:54),
	TCCATGACGTCTTTGATGTT	(SEQ ID NO:55),
	TCCATGACGTATTTGATGTT	(SEQ ID NO:56), and
	TCCATGACGTGTTTGATGTT	(SEQ ID NO:57).

**Figure 1**  
**(1/3)**

feline	MGPCHGALHPLSLVQAAALAVALAAGTLPFAFLPCELQRHGLVNCNDWFLKSVPHFSAAA	60
canine	MGPCRGALHPLSLVQAAALALALAAGTLPFAFLPCELOPHGLVNCNWFLKSVPRFSAAA	60
bovine	MGP-YCAPHPLSLVQAAALAAALAEGLTPAFLPCELOPHGQVDNCNWFLKSVPHFSAGA	59
mouse	MGP-YCAPHPLSLVQAAALAAALAEGLTPAFLPCELOPHGQVDNCNWFLKSVPHFSAGA	59
ovine	MGP-YCAPHPLSLVQAAALAAALAEGLTPAFLPCELOPHGRGVNCNWFLKSVPRFSAGA	59
porcine	MGP-RCTLHPLSLVQVTALAAALAQGRIPAFLLPCELOPHGLVNCNWFLKSVPHFSAAA	59
horse	MGPCHGALQPLSLVQAAMLAVALAAGTLPPFLLPCELOPHGLVNCNWFLKSVPHFSAAA	60
human	MGFCSRSLHPLSLVQAIMLAMLTALGTLPFAFLPCELOPHGLVNCNWFLKSVPHFSMAA	60
rat	MVLCCRTHLPLSLVQAALEALAGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAAE	60
	* : :*****. ** : * * *.*****: ; * *:*****.*** .	
feline	PRGNVTSLSLYSNRIHHLHSDSFVHLSSLRRLNLKWNCPPASLSPMHFPCMTIEPTFTL	120
canine	PRGNVTSLSLYSNRIHHLDYDFVHFVHLRRLNLKWNCPPASLSPMHFPCMTIEPTFTL	120
bovine	PRANVTSLSLISNRIHHLHSDSFVHLSNLRVLNLKWNCPPAGLSPMHFFCRMTIEPTFTL	119
mouse	PRANVTSLSLISNRIHHLHSDSFVHLSNLRVLNLKWNCPPAGLSPMHFFCRMTIEPTFTL	119
ovine	PRANVTSLSLISNRIHHLHSDSFVHLSNLRVLNLKWNCPPAGLSPMHFFCRMTIEPTFTL	119
porcine	PRANVTSLSLISNRIHHLHSDSFVHLSSLRTLNELKWNCPPAGLSPMHFPCMTIEPTFTL	119
horse	PRDNVTSLSLHLSNRIHHLHSDSFAQLSNLKLKWNCPPAGLSPMHFFCRMTIEPTFTL	120
human	PRGNVTSLSLSSNRIHHLHSDSFAHLPSLRHLNLKWNCPPVGLSPMHFFPCMTIEPTFTL	120
rat	PRSNTITSLSLIANRIHHLHNLDVFHLPNVRQLNLKWNCPPGSLPHFSCRMTEPKFTL	120
	** *:***** :*****: **.:: :: ***** .***:*:.***** ***	
feline	AVPTLEEENLSYSNITTVPALPSSLVLSLSRSTNILVDPANLAGLSRFLFDGNCYY	180
canine	AVPTLEDNLNSYSNITTVPALPSSLVLSLSRSTNILVDPATLAGLYALRFLFDGNCYY	180
bovine	AVPTLEEENLSYNGITTVPALPSSLVLSLSHSITSILVLGPTHFTGLHALRFLYMDGNCYY	179
mouse	AVPTLEEENLSYNGITTVPALPSSLVLSLSHSITSILVLGPTHFTGLHALRFLYMDGNCYY	179
ovine	AVPTLEEENLSYNGITTVPALPSSLVLSLSHSITSILVLGPTHFTGLHALRFLYMDGNCYY	179
porcine	AVPTLEEENLSYSNITTVPALPDSLVLSLSRSTNILVDPHTLGLHALRYLYMDGNCYY	179
horse	AVPTLEEENLSYNGITTVPALPSSLVLSLSRSTNILVDPHTLGLHALRFLYMDGNCYY	180
human	AVPTLEEENLSYNIMTTVPALPKSLISLSHSITNILMDSASLAGLHALRFLYMDGNCYY	180
rat	AMRMLEEENLSYNGITTVPRLPSSLTNLSHTNILVDAASSLAGLHARVLFDGNCYY	180
	*: *.*****.* *** *.** *.**.*.***.***.: :*:**:** *:*****	
feline	KNPCPQALQVAPGALLGLGNLTHLSLKYNLTAVERGPLPSSLEYLLSYNHIIITLAPEDL	240
canine	KNPCQQALQVAPGALLGLGNLTHLSLKYNLTVPVPGRLPSSLEYLLSYNHIIITLAPEDL	240
bovine	MNPCPRALEVAPGALLGLGNLTHLSLKYNLTVEPRRLPPLDITLLSYNHIVTLAPEDL	239
mouse	MNPCPRALEVAPGALLGLGNLTHLSLKYNLTVEPRRLPPLDITLLSYNHIVTLAPEDL	239
ovine	KNPCQQALEVAPGALLGLGNLTHLSLKYNLTVEPRRLPPLDITLLSYNHIIITLAPEDL	239
porcine	KNPCQGALEVAPGALLGLGNLTHLSLKYNLTVEPRRLPPLSEYLLSYNHIVTLAPEDL	239
horse	KNPCGRALEVAPGALLGLGNLTHLSLKYNLTTPVRSPLPSSLEYLLSYNHIVTLAPEDL	240
human	KNPCRQALEVAPGALLGLGNLTHLSLKYNLTVPVRNLPSSLEYLLSYNRIVKLAPEDL	240
rat	KNPCNGAVNVTPDAFLGLSNLTHLSLKYNLTVEPRQLPSSLEYLLSYNLIVKLGAEIDL	240
	*** *:*.**.****.***** **** *.**.*: ***** *:.*.***	
feline	ANLTALRVLDVGNCRRCDHARNPCMECPKGFPPLHPDTFSHLNHLEGLVLKDSSLYNLN	300
canine	ANLTALRVLDVGNCRRCDHARNPCRECPKGFPLHPDTFGHLSHLEGLVLKDSSLYSLD	300
bovine	ANLTALRVLDVGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSSLYKLE	299
mouse	ANLTALRVLDVGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSSLYKLE	299
ovine	ANLTALRVLDVGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSSLYKLE	299
porcine	ANLTALRVLDVGNCRRCDHARNPCRECPKHFPKLHSDTFSHLSRLEGLVLKDSSLYNLD	299
horse	ANLTALRVLDVGNCRRCDHARNPCVECPHKFPQLHSDTFSHLSRLEGLVLKDSSLYQLN	300
human	ANLTALRVLDVGNCRRCDHARNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLYSWLN	300
rat	ANLTSRLMLDVGNCRRCDHADPDLCTECROKSLDLHPQTFHHLHLEGLVLKDSSLSHSLN	300
	***:*:.***** ***** : * ** : ..*:.** *.*****:***** *::	
feline	PRWFHALGNLMVLDLSENFLYDCITTKTKAFQGLAQLRRNLNLSFNHYKKVSFAHLHLAPSF	360
canine	PRWFHGLGNLMVLDLSENFLYDCITTKTKAFYGLARLRRNLNLSFNHYKKVSFAHLHLASSF	360
bovine	KDWFRGLGRLQVLDLSENFLYDYITTKTIENDLTQLRRNLNLSFNHYKKVSFAHLHLASSF	359
mouse	KDWFRGLGRLQVLDLSENFLYDYITTKTIENDLTQLRRNLNLSFNHYKKVSFAHLHLASSF	359
ovine	KDWFRGLGRLQVLDLSENFLYDYITTKTIERNLTQLRRNLNLSFNHYKKVSFAHLQLAPSF	359
porcine	TRWFRGLDRQLVLDLSENFLYDCITTKTKAFQGLARLRSNLNLSFNHYKKVSFAHLHLAPSF	359
horse	PRWFRGLGNLTVDLSENFLYDCITTKTKAFQGLAQLRRNLNLSFNHYKKVSFAHLT LAPSF	360
human	ASWFRGLGNLRVLDLSENFLYKCIITTKTKAFQGLTQLRKLNLSFNHYQKVSFAHL SLAPSF	360
rat	SKWFOGLANLSVLDLSENFLYESINKTSFAQNLTRLRLKDLNLSFNHYCKVVSFAHLHLASSF	360
	***.*.***** ***** * * * * .....***** *****:***** *	



**Figure 1**  
**(2/3)**

[illegible]

feline	SFFALATRLRELNLSANALKTVEPSWFGSLAGTLKVLDVTGNPLHCACGAAFVDFLLEQV	778
canine	SFFALAVRLRELNLSANALKTVEPSWFGSLAGALKVLDTVANPLHCACGATFVDLFLEQV	780
bovine	GFFVRATRLLIELNLSANALKTVDPSPWFGSLAGTLKILDVSANPLHCACGAAFVDFLLERQ	776
mouse	GFFVRATRLLIELNLSANALKTVDPSPWFGSLAGTLKILDVSANPLHCACGAAFVDFLLERQ	776
ovine	GFFVLARNLKELNLSANALKTVDPSPWFGRLTETNLILDVSANPLHCACGAAFVDFLLEMQ	776
porcine	GFFALAKQLEELNLSANALKTVEPSWFGSMVGNLKVLDVSANPLHCACGATFVGFLLEQV	777
horse	GFFALATRLRELNLSANALKTEEPSPWFGFLAGSLLEVLDVSANPLHCACGAAFVDFLLQVQ	778
human	GFFSKAKELRELNLSANALKTVDSWFPGPLASALQILDVDSANPLHCACGAAFMDFLLEQV	778
rat	AFFALAVELKEVNLSHNILKTVPDWSWFGPIVMNLTVLDDSSNPPLHCACGAAPFDLLLLEQV	779
	. ** * . * : *** * * : * : * : * : * : * : * : * : * : *	
feline	AAVPGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCCFG	838
canine	AAVPGLPSPRVKCGSPGQLQGRSIFAQDLRLCLDEALSWCFS	840
bovine	EAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETLSLDCFG	836
mouse	EAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETLSLDCFG	836
ovine	AAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETLSLDCFG	836
porcine	AAVPGLPSPRVKCGSPGQLQGRSIFAQDLRLCLDETLSWNCFG	837
horse	AAVPGLPSPRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFG	838
human	AAVPGLPSPRVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCAF	838
rat	TKVPGLANGVKCSPRQLQGRSIFAQDLRLCLDDVLSRDCCFG	839
	****. * . **** * * * : *****. * * * : * : * : * : * : *	
feline	CGWDLWYCFHLC LAWLPRRGRR--RGADALPYDAFVVFDKAQS AVADWVYNELRVLEER	896
canine	CGWDLWYCFHLC LAWLPRRGRR--RGVDALAYDAFVVFDKAQSS VADWVYNELRVQLEER	898
bovine	CGWDLWYCFHLC LAHLPRRRRQ--RGEDTLLYDAVVVF DKKVQSAVADWVYNELRVQLEER	894
mouse	CGWDLWYCFHLC LAHLPRRRRQ--RGEDTLLYDAVVVF DKKVQSAVADWVYNELRVQLEER	894
ovine	CGWDLWYCFHLC LAHLPRRRRQ--RGEDTLLYDAFVVFDKAQSAVADWVYNELRVQLEER	894
porcine	CGWDLWYCFHLC LAWLPHRGQR--RGADALFYDAFVVFDKAQSAVADWVYNELRVQLEER	895
horse	CGWDLWYCFHLC LAWLPRRGWQ--RGADALS YDAFVVFDKAQSAVADWVYNELRVLEER	896
human	CGWDLWYCFHLC LAWLFWRGQRSGRDEDALPYDAFVVFDKTS AVADWVYNELRGQLEEC	898
rat	CGWDVWYCFHLC LAWLPLLTRGR-RSAQALPYDAFVVFDKAQSAVADWVYNELRVLEER	898
	*****:***** ** ** *. : * * *,*****. **:***** :***	
feline	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDRVSGLLRAS FLLAQORL	956
canine	RGRRALRLCLEERDWVPGKTLFENLWASVYSSRKTFVLAHTDRVSGLLRAS FLLAQORL	958
bovine	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKTMFVLDHTDRVSGLLRAS FLLAQORL	954
mouse	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKTMFVLDHTDRVSGLLRAS FLLAQORL	954
ovine	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKTMFVLDHTDRVSGLLRAS FLLAQORL	954
porcine	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKTFVLAHTDRVSGLLRAS FLLAQORL	955
horse	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDQVSGLLRAS FLLAQORL	956
human	RGRWALRLCLEERDWLPGKTLFENLWASVYGSRKTFVLAHTDRVSGLLRAS FLLAQORL	958
rat	RGRRALRLCLEERDWLPGQTLENLWASIYGSRKTFVLAHTDKVSGLLRTS FLLAQORL	958
	*** *****:***:**:*****:*.*** :*** :*:*****:*****	
feline	LEDKRDVVVLVILRPDAHR SRVRLRQRLCRQSVLLWPHQP SGQSFWAQLGTALTRDNQ	1016
canine	LEDKRDVVVLVILCPDAHR SRVRLRQRLCRQSVLLWPHQP SGQSFWAQLGTALTRDNR	1018
bovine	LEDKRDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQP SGQGSEWANLGIALTRDNR	1014
mouse	LEDKRDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQP SGQGSEWANLGIALTRDNR	1014
ovine	LEDKRDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQP SGQGSEWANLGIALTRDNR	1014
porcine	LEDKRDVVVLVILRPDAYRSRYVRLRQRLCRQSVLLWPHQP SGQSFWAQLGTALTRDNH	1015
horse	LEDKRDVVVLVILSPDARRSRVRLRQRLCRQSVLLWPHQP SGQSFWAQLGMALTRDNR	1016
human	LEDKRDVVVLVILSPDGRRSRVRLRQRLCRQSVLLWPHQP SGQSFWAQLGMALTRDNR	1018
rat	LEDKRDVVVLVILRPDAHR SRVRLRQRLCRQSVLLWPHQP NGQSFWAQLGTALTRDNH	1018
	***** * . *****:***** ** *****:*. *****:	
feline	HFYNQNFCRGPTTAE-----	1031
canine	HFYNQNFCRGPTTA-----	1032
bovine	HFYNRNFCRGPTTAE-----	1029
mouse	HFYNRNFCRGPTTAE-----	1032
ovine	HFYNRNFCRGPTTAE-----	1029
porcine	HFYNRNFCRGPTTAE-----	1030
horse	HFYNQNFCRGPTMAE-----	1031
human	HFYNRNFCQGPTAE-----	1032
rat	HFYNRNFCRGPTAE-----	1032
	****.****.***	

Figure 2

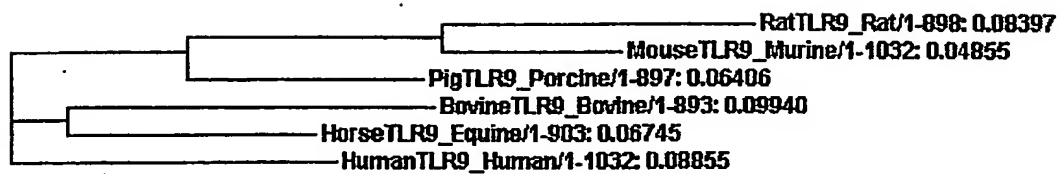
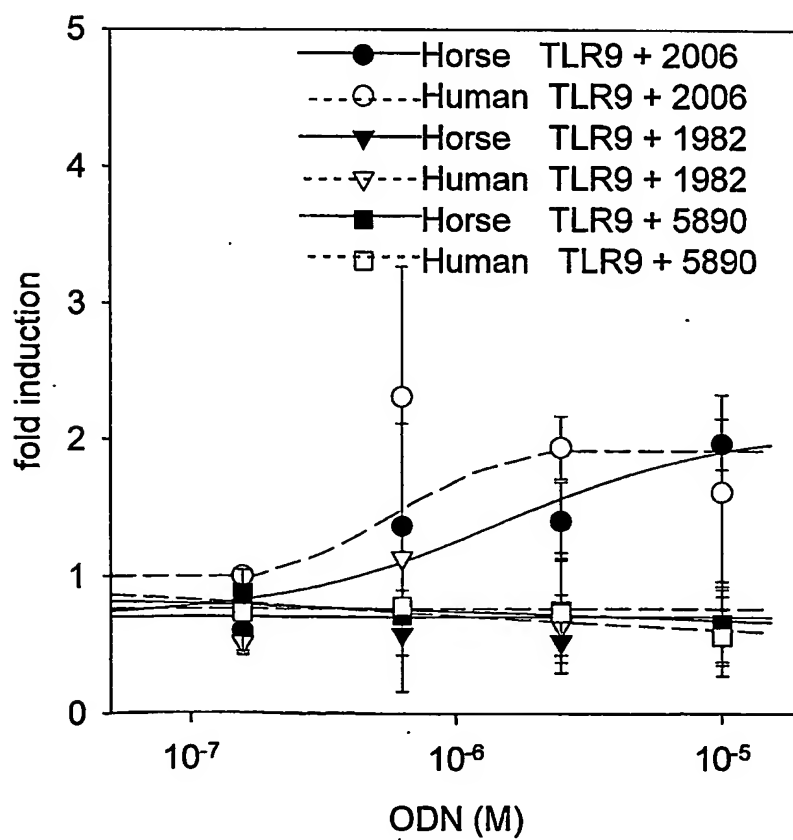


Figure 3



## SEQUENCE LISTING

<110> Coley Pharmaceutical GmbH  
University of Saskatchewan  
Qiagen GmbH

<120> TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES

<130> C1041.70040WO00

<150> US 60/412,479

<151> 2002-09-19

<160> 70

<170> PatentIn version 3.1

<210> 1

<211> 1032

<212> PRT

<213> Rattus norvegicus

<400> 1

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
1 5 10 15

Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe  
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn  
50 55 60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn  
65 70 75 80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp  
85 90 95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met  
100 105 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu  
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
130 135 140

Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
 145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro  
 180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser  
 260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe  
 290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu  
 325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala  
 340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu  
 355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu  
 370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala  
 405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr  
 420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val  
 435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser  
 450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu  
 465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu  
 485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala  
 500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp  
 515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu  
 530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe  
 545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser  
 565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val  
 580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly  
 595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe

-4-

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Thr Arg Gly Arg Arg Ser  
 850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln  
 865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu  
 885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp  
 900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr  
 915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Lys Val Ser  
 930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His  
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
 980 985 990

Leu Phe Trp Pro His Gln Pro Asn Gly Gln Gly Ser Phe Trp Ala Gln  
 995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg  
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu  
 1025 1030

<210> 2  
 <211> 821  
 <212> PRT  
 <213> Rattus norvegicus

<400> 2

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15



Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe  
                   20                                  25                                  30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
                   35                                  40                                  45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn  
                   50                                  55                                  60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn  
                   65                                  70                                  75                                  80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp  
                                   85                                  90                                  95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met  
                                   100                                  105                                  110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu  
                   115                                  120                                  125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
                   130                                  135                                  140

Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
                   145                                  150                                  155                                  160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly  
                                   165                                  170                                  175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro  
                   180                                  185                                  190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
                   195                                  200                                  205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
                   210                                  215                                  220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu  
                   225                                  230                                  235                                  240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg  
                                   245                                  250                                  255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser  
 260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe  
 290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu  
 325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala  
 340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu  
 355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu  
 370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala  
 405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr  
 420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val  
 435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser  
 450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu  
 465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu  
 485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala  
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp  
515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu  
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe  
545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser  
565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val  
580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly  
595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe  
610 615 620

Phe Gln Asp Leu Arg Ser Leu Ile His Leu Asp Leu Ser Gln Asn Lys  
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asn Tyr Leu Pro Lys Ser Leu  
645 650 655

Thr Lys Leu Ser Phe Arg Asp Asn His Leu Ser Phe Phe Asn Trp Ser  
660 665 670

Ser Leu Ala Phe Leu Pro Asn Leu Arg Asp Leu Asp Leu Ala Gly Asn  
675 680 685

Leu Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu  
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Phe Val Val Pro Ala  
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn

[illegible]

gcccccgacc tctgtacaga atgccggcag aagtcccttg atctgcaccc tcagactttc 840  
 catcacctga gccaccttga aggcctgggtg ctgaaggaca gttctctcca ctcgctgaac 900  
 tccaagtggg tccaggggtct ggcgaacctc tcgggtgctgg acctaagcga gaactttctc 960  
 tacgagagca tcaacaaaac cagcgccttt cagaacctga cccgtctgcg caagctcgac 1020  
 ctgtccttca attactgcaa gaaggatcg ttcgcccgcc tccacctggc aagttccttc 1080  
 aagagcctgg tgcgctgca ggagctgaac atgaacggca tcttcttccg cttactcaac 1140  
 aagaacacgc tcaggtgggt ggtgggtctg cccaagctcc acacgctgca ctttcaaagt 1200  
 aatttcatca accaggcgca gctcagcgtc tttagtacct tccgagccct tcgctttgtg 1260  
 gacctgtcca ataatcgcat cagcgggcct ccaacgctgt ccagagtcgc ccccgaaaag 1320  
 gcgacgagg cggaagaagg ggttccatgg cctgcaagtc tcaccccagc tctcccagc 1380  
 actcccgctc caaagaactt catggtcagg tgtaagaacc tcagattcac catggacctg 1440  
 tctcggaaca accaggtgac tatcaagcca gagatgttcg tcaacctctc ccatctccag 1500  
 tgtctgagcc tgagccacaa ctgcatcgcg caggctgtca atggctctca gttcctgccc 1560  
 ctgaccaacc tgaagggtgt ggacctgtcc tataacaagc tggacctgta ccattcgaaa 1620  
 tcgttcagtg agtcccaca gttgcaggcc ctggacctga gctacaacag ccagccattc 1680  
 agcatgcagg ggataggcca caacttcagt tttctggcca atctgtccag gttacagaac 1740  
 cttagcctgg cacacaatga cattcacagc cgcgtgtcct cagcctcta cagcacctca 1800  
 gtggagtatc tggacttcag cggcaacggt gtggggccgca tgtgggacga ggaggacctt 1860  
 tacctctatt tcttccaaga cctgagaagc ctgattcatc tggacctgtc tcagaataag 1920  
 ctgcacatcc tccggcccca gaacctcaac tacctcccca agagcctgac gaagctgagt 1980  
 ttccgtgaca atcacctctc tttctttaac tggagcagtc tggccttcct gcccaatctg 2040  
 cgagacctgg acctggcagg caatctacta aaggccctga ccaacggcac cctgcctaatt 2100  
 ggcaacgtcc tccagaaact ggatgtcagt agcaacagta tcgtctttgt ggtcccagcc 2160  
 ttctttgctc tggcggtaga gctaaaagag gtcaacctca gccataacat cctcaagact 2220  
 gtggatcgct cctggtttgg gccattgtg atgaacctga cggttctaga cgtgagcagc 2280  
 aacctctgc attgtgcctg cgggtgcaccc tttgtagact tactgctgga agtgcagacc 2340  
 aagggtgctg gcctggctaa cgggtgtgaag tgtggcagtc cccgccagct gcagggccgc 2400  
 agcatctttg cgcaagacct gcggtgtgtc ctggatgacg tcctttctcg ggactgcttt 2460  
 ggcctttcac tcctggctgt ggcctgtggc acggtgttgc ctttactgca gcattctctgc 2520  
 ggctgggacg tctggtactg tttccatctg tgccctggcat ggctaccttt gctgacctgc 2580

ggccggcgca ggcgccaagc tctcccttat gatgccttcg tgggtgttcga taaggcgag 2640  
 agcgcggttg ctgactgggt gtataacgag cttcgagtgc ggctagagga gcggcgcggt 2700  
 cgccgagccc tacgcttggt tctggaggac cgagattggc tgcttgcca gacactcttc 2760  
 gagaacctct gggcctccat ctatggcagc cgcaagactc tgtttgtgct ggcccacacg 2820  
 gacaaggtca gtggcctcct ggcaccagc ttctgtctgg ctcagcagcg cctgctggag 2880  
 gaccgcaagg acgtgggtgt gttggtgatc ctgcgcctg atgcccaccg ctcccgctac 2940  
 gtgcgactgc gccagcgctt ctgcgcagc agtgtgtctt tctggcccca tcagcccaac 3000  
 gggcagggca gcttctgggc ccagctgagt acagccctga ctagggacaa ccaccacttc 3060  
 tataaccgga acttctgccc gggacctaca gcagaatag 3099

<210> 4  
 <211> 2463  
 <212> DNA  
 <213> Rattus norvegicus

<400> 4  
 atggttctct gtgcaggac cctgcacccc ttgtctctcc tgggtacaggc cgcagtgtctg 60  
 gctgaggctc tggccctggg taccctgcct gccttcctac cctgtgaact gaagcctcat 120  
 ggcttggtag actgcaactg gctcttctct aagtctgtgc ctcacttctc tgccgcagaa 180  
 cccggttcca acatcaccag cctttccttg atcgccaacc gcatccacca cctgcacaac 240  
 ctcgactttg tccacctgcc caacgtgcga cagctgaacc tcaagtggaa ctgtccgccc 300  
 cctggcctca gcccttgca cttctcctgc cgcattacca ttgagcccaa aaccttctctg 360  
 gctatgcgca tgctggaaga gctgaacctg agctataacg gtatcaccac tgtgccccgc 420  
 ctgcccagct ccctgacgaa tctgagccta agccacacca acatcctggg actcgatgcc 480  
 agcagcctcg ctggcctgca cagcctgcga gttctcttca tggacgggaa ctgctactac 540  
 aagaaccctt gcaacggggc ggtgaacgtg acccgggacg ccttctctggg cttgagcaac 600  
 ctcaccactt tgtcccttaa gtataacaac ctcacagagg tgccccgcca actgcccccc 660  
 agcctggagt acctcctgct gtctataaac ctcactgtca agctgggggc cgaagaccta 720  
 gccaacctga cctcccttcg aatgcttgat gtgggtggga attgccgtcg ctgtgatcac 780  
 gccccgacc tctgtacaga atgcccagc aagtcccttg atctgcaccc tcagactttc 840  
 catcacctga gccaccttga aggcctgggt ctgaaggaca gttctctcca ctcgctgaac 900  
 tccaagtggg tccaggggtt ggcgaacctc tgggtgctgg acctaaagcga gaactttctc 960  
 tacgagagca tcaacaaaac cagcgccttt cagaacctga cccgtctgcg caagctcgac 1020

```

ctgtccttca attactgcaa gaaggatcgc ttcgcccgcg tccacctggc aagttccttc 1080
aagagcctgg tgctcgtgca ggagctgaac atgaacggca tcttcttccg cttactcaac 1140
aagaacacgc tcaggtggct ggctggctctg cccaagctcc acacgctgca ccttcaaattg 1200
aatttcatca accaggcgca gctcagcgtc tttagtacct tccgagccct tcgctttgtg 1260
gacctgtcca ataatcgcat cagcgggcct ccaacgctgt ccagagtcgc ccccgaaaag 1320
gcagacgagg cggagaaggg ggttccatgg cctgcaagtc tcaccccagc tctcccagagc 1380
actcccgctc caaagaactt catggtcagg tgtaagaacc tcagattcac catggacctg 1440
tctcggaaaca accaggtgac tatcaagcca gagatgttcg tcaacctctc ccatctccag 1500
tgtctgagcc tgagccacaa ctgcatcgcg caggctgtca atggctctca gttcctgccc 1560
ctgaccaacc tgaaggtgct ggacctgtcc tataacaagc tggacctgta ccattcgaaa 1620
tcgttcagtg agctcccaca gttgcaggcc ctggacctga gctacaacag ccagccattc 1680
agcatgcagg ggataggcca caacttcagt tttctggcca atctgtccag gttacagaac 1740
cttagcctgg cacacaatga cattcacagc cgcgtgtcct cagcctcta cagcacctca 1800
gtggagtatc tggacttcag cggcaacggt gtgggccgca tgtgggacga ggaggacctt 1860
tacctctatt tcttccaaga cctgagaagc ctgattcacc tggacctgtc tcagaataag 1920
ctgcacatcc tccggcccca gaacctcaac tacctcccca agagcctgac gaagctgagt 1980
ttccgtgaca atcacctctc tttctttaac tggagcagtc tggccttcct gcccaatctg 2040
cgagacctgg acctggcagg caatctacta aaggccctga ccaacggcac cctgcctaatt 2100
ggcacgctcc tccagaaact ggatgtcagt agcaacagta tcgtctttgt ggtcccagcc 2160
ttctttgctc tggcggtaga gctaaaagag gtcaacctca gccataacat cctcaagact 2220
gtggatcgct cctggtttgg gccattgtg atgaacctga cggttctaga cgtgagcagc 2280
aaccctctgc attgtgcctg cgggtgaccc tttgtagact tactgctgga agtgcagacc 2340
aagggtgctg gcctggctaa cgggtgtgaag tgtggcagtc cccgccagct gcagggccgc 2400
agcatctttg cgcaagacct gcggtgtgtc ctggatgacg tcctttctcg ggactgcttt 2460
ggc

```

```

<210> 5
<211> 1030
<212> PRT
<213> Sus scrofa

<400> 5

```

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val  
 1 5 10 15  
 Thr Ala Leu Ala Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu  
 20 25 30  
 Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe  
 35 40 45  
 Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val  
 50 55 60  
 Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80  
 Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn  
 85 90 95  
 Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr  
 100 105 110  
 Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
 115 120 125  
 Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu  
 130 135 140  
 Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr  
 145 150 155 160  
 His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn  
 165 170 175  
 Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly  
 180 185 190  
 Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205  
 Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu  
 210 215 220  
 Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala  
 225 230 235 240



Asn	Leu	Thr	Ala	Leu	Arg	Val	Leu	Asp	Val	Gly	Gly	Asn	Cys	Arg	Arg
				245					250					255	
Cys	Asp	His	Ala	Arg	Asn	Pro	Cys	Arg	Glu	Cys	Pro	Lys	Asp	His	Pro
			260					265					270		
Lys	Leu	His	Ser	Asp	Thr	Phe	Ser	His	Leu	Ser	Arg	Leu	Glu	Gly	Leu
		275					280					285			
Val	Leu	Lys	Asp	Ser	Ser	Leu	Tyr	Asn	Leu	Asp	Thr	Arg	Trp	Phe	Arg
	290					295					300				
Gly	Leu	Asp	Arg	Leu	Gln	Val	Leu	Asp	Leu	Ser	Glu	Asn	Phe	Leu	Tyr
305					310					315					320
Asp	Cys	Ile	Thr	Lys	Thr	Thr	Ala	Phe	Gln	Gly	Leu	Ala	Arg	Leu	Arg
				325					330					335	
Ser	Leu	Asn	Leu	Ser	Phe	Asn	Tyr	His	Lys	Lys	Val	Ser	Phe	Ala	His
			340					345					350		
Leu	His	Leu	Ala	Pro	Ser	Phe	Gly	His	Leu	Arg	Ser	Leu	Lys	Glu	Leu
		355					360					365			
Asp	Met	His	Gly	Ile	Phe	Phe	Arg	Ser	Leu	Ser	Glu	Thr	Thr	Leu	Gln
	370					375					380				
Pro	Leu	Val	Gln	Leu	Pro	Met	Leu	Gln	Thr	Leu	Arg	Leu	Gln	Met	Asn
385					390					395					400
Phe	Ile	Asn	Gln	Ala	Gln	Leu	Ser	Ile	Phe	Gly	Ala	Phe	Pro	Gly	Leu
				405					410					415	
Leu	Tyr	Val	Asp	Leu	Ser	Asp	Asn	Arg	Ile	Ser	Gly	Ala	Ala	Arg	Pro
			420					425					430		
Val	Ala	Ile	Thr	Arg	Glu	Val	Asp	Gly	Arg	Glu	Arg	Val	Trp	Leu	Pro
		435					440					445			
Ser	Arg	Asn	Leu	Ala	Pro	Arg	Pro	Leu	Asp	Thr	Leu	Arg	Ser	Glu	Asp
	450					455					460				
Phe	Met	Pro	Asn	Cys	Lys	Ala	Phe	Ser	Phe	Thr	Leu	Asp	Leu	Ser	Arg
465					470					475					480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg  
 485 490 495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn  
 500 505 510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser  
 515 520 525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro  
 530 535 540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met  
 545 550 555 560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu  
 565 570 575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln  
 580 585 590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp  
 595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln  
 610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His  
 625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His  
 645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu  
 660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu  
 675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg  
 690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe

705	710	715	720
Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu	725	730	735
Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys	740	745	750
Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr	755	760	765
Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro	770	775	780
Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile	785	790	795
Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn	805	810	815
Cys Phe Gly Ile Ser Leu Leu Ala Met Ala Leu Gly Leu Val Val Pro	820	825	830
Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu	835	840	845
Cys Leu Ala Trp Leu Pro His Arg Gly Gln Arg Arg Gly Ala Asp Ala	850	855	860
Leu Phe Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val	865	870	875
Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg	885	890	895
Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro	900	905	910
Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg	915	920	925
Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu	930	935	940

Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys  
 945 950 955 960

Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala Tyr Arg Ser Arg  
 965 970 975

Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp  
 980 985 990

Pro His Gln Pro Arg Gly Gln Gly Ser Phe Trp Ala Gln Leu Gly Thr  
 995 1000 1005

Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg Asn Phe Cys  
 1010 1015 1020

Arg Gly Pro Thr Thr Ala Glu  
 1025 1030

<210> 6  
 <211> 819  
 <212> PRT  
 <213> Sus scrofa

<400> 6

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val  
 1 5 10 15

Thr Ala Leu Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu  
 20 25 30

Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe  
 35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val  
 50 55 60

Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80

Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn  
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr  
 100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
 115 120 125

Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu  
 130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr  
 145 150 155 160

His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn  
 165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly  
 180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205

Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu  
 210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala  
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro  
 260 265 270

Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg  
 290 295 300

Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320

Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg  
 325 330 335

Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln  
 370 375 380

Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu  
 405 410 415

Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430

Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro  
 435 440 445

Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp  
 450 455 460

Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg  
 465 470 475 480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg  
 485 490 495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn  
 500 505 510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser  
 515 520 525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro  
 530 535 540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met  
 545 550 555 560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu  
 565 570 575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln  
 580 585 590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp  
 595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln  
 610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His  
 625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His  
 645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu  
 660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu  
 675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg  
 690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe  
 705 710 715 720

Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu  
 725 730 735

Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys  
 740 745 750

Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr  
 755 760 765

Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro  
 770 775 780

Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile  
 785 790 795 800

Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn  
 805 810 815

Cys Phe Gly

<210> 7  
 <211> 3352  
 <212> DNA  
 <213> Sus scrofa

<400> 7  
 gagcacgaac atccttcact gtagctgctg cccggctctgc cagccagacc ctttggagaa 60  
 gacccactc cctgtcatgg gccccgctg caccctgcac cccctttctc tcctgggtgca 120  
 ggtgacagcg ctggctgcgg ctctggcca gggcaggctg cctgccttcc tgccctgtga 180  
 gctccagccc cacggcctgg tgaactgcaa ctggctcttc ctgaagtccg tgccccactt 240  
 ctgggaggca ggcggcgagg ccaacgtcac cagcctctcc ttactctcca accgcatcca 300  
 ccacctgcac gactccgact tcgtccacct gtccagccta cgaactctca acctcaagtg 360  
 gaactgcccg cgggctggcc tcagcccat gcacttcccc tgccacatga ccatogagcc 420  
 caacaccttc ctggcgtgc ccacctgga ggagctgaac ctgagctaca acagcatcac 480  
 gaccgtgcct gccctgcccg actccctcgt gtccctgtcg ctgagccgca ccaacatcct 540  
 ggtgctagac cccaccacc tcactggcct acatgccctg cgctacctgt acatggatgg 600  
 caactgctac tacaagaacc cctgccaggg ggcgctggag gtggtgccgg gtgccctcct 660  
 cggcctgggc aacctcacac atctctcact caagtacaac aatctcacgg aggtgccccg 720  
 cagcctgccc cccagcctgg agacctgct gttgtcctac aaccacattg tcacctgac 780  
 gcctgaggac ctggccaatc tgactgcct gcgcgtgctt gatgtggggg ggaactgccg 840  
 ccgctgtgac catgcccga acccctgcag ggagtgcca aaggaccacc ccaagctgca 900  
 ctctgacacc ttcagccacc tgagccgcct cgaaggcctg gtgttgaaag acagttctct 960  
 ctacaacctg gacaccaggt gggtccgagg cctggacagg ctccaagtgc tggacctgag 1020  
 tgagaacttc ctctacgact gcatcaccaa gaccacggcc ttccagggcc tggcccgact 1080  
 gcgcagcctc aacctgtcct tcaattacca caagaagggt tcctttgccc acctgcacct 1140  
 ggcacctcc tttgggcacc tccggctcct gaaggagctg gacatgcatg gcatcttctt 1200  
 ccgctcgctc agtgagacca cgctccaacc tctgggtcaa ctgcctatgc tccagacct 1260  
 gcgcctgcag atgaacttca ttaaccagga ccagctcagc atctttgggg ccttccctgg 1320  
 cctgctgtac gtggacctat cggacaaccg catcagcgga gctgcaaggc cagtggccat 1380  
 tactagggag gtggatggta gggagagggt ctggctgcct tccaggaacc tcgctccacg 1440  
 tccactggac actctccgct cagaggactt catgccaaac tgcaaggcct tcagcttcac 1500



cttggacctg tctcggaaca acctggtgac aatccagtcg gagatgtttg ctgcctctc 1560  
 acgcctcgag tgccctgcgc tgagccacaa cagcatctcc caggcggta atggctctca 1620  
 gtttgtgccc ctgaccagcc tgcgggtgct ggacctgtcc cacaacaagc tggacctgta 1680  
 tcacgggcgc tcgttcacgg agctgccgcg cctggaagca ctggacctca gctacaatag 1740  
 ccagcccttt accatgcagg gtgtgggcca caacctcagc ttcgtggccc agctgcccgc 1800  
 cctgcgctac ctacgcctgg cgcacaatga catccatagc cgagtgtccc agcagctctg 1860  
 tagcgctca ctgtgcgccc tggacttttag cggcaacgat ctgagccgga tgtgggctga 1920  
 gggagacctc tatctccgct tcttccaagg cctaagaagc ctagtctggc tggacctgtc 1980  
 ccagaaccac ctgcacaccc tctgtccacg tgccctggac aacctccca aaagcctgaa 2040  
 gcatctgcat ctccgtgaca ataacctggc cttcttcaac tggagcagcc tgacctcct 2100  
 gccaagctg gaaacctgg acttggtgg aaaccagctg aaggccctaa gcaatggcag 2160  
 cctgccatct ggcacccagc tgcggaggct ggacctcagt ggcaacagca tcggctttgt 2220  
 gaacctggc tcttttgccc tggccaagca gttagaagag ctcaacctca gcgccaatgc 2280  
 cctcaagaca gtggagccct cctggtttgg ctcgatggtg ggcaacctga aagtcctaga 2340  
 cgtgagcgcc aacctctgc actgtgcctg tggggcgacc ttcgtgggct tcctgctgga 2400  
 ggtacaggct gccgtgcctg ggctgccag ccgcgtcaag tgtggcagtc cggggcagct 2460  
 ccagggccat agcatctttg cgcaagacct gcgcctctgc ctggatgaga ccctctctg 2520  
 gaactgtttt ggcatctgc tgctggccat ggccctgggc ctgggtgtgc ccatgctgca 2580  
 ccacctctgc ggctgggacc tctggtactg cttccacctg tgctggcct ggctgcccc 2640  
 ccgagggcag cggcggggcg cagacgccct gttctatgat gccttcgtgg tctttgacaa 2700  
 agctcagagt gctgtggccg actgggtgta caacgagctg cgggtgcagc tggaggagcg 2760  
 ccgtgggcgc cgcgcactgc gcctgtgcct ggaggagcga gactggttac ctggcaagac 2820  
 gctcttcgag aacctgtggg cctcagtcta cagcagccgc aagacctgt ttgtgctggc 2880  
 ccacacggac cgtgtcagcg gcctcttgcg tgccagttc ctgctggccc agcagcgct 2940  
 gctggaggac cgcaaggacg ttgtagtgct ggtgatcctg cgcctcgatg cctaccgctc 3000  
 ccgctacgtg cggctgcgc agcgctctg ccgccagagt gtctctctc ggccccacca 3060  
 gcccgtggg cagggcagct tctgggcca gctgggcaca gccctgacca gggacaacca 3120  
 ccacttctat aaccggaact tctgccgggg cccacgaca gccgaatagc actgagtgc 3180  
 agcccagttg cccagcccc cctggatttg cctctctgcc tggggtgccc caacctgctt 3240  
 tgctcagcca caccactgct ctgctccctg tccccaccc cccccccag cctggcatgt 3300

aacatgtgcc caataaatgc taccggaggg ccaagaaaaa aaaaaaaaaa aa 3352

<210> 8

<211> 2457

<212> DNA

<213> Sus scrofa

<400> 8

atgggcccc gctgcaccct gcacccctt tctctcctgg tgcaggtgac agcgctggct 60  
 gcggctctgg ccagggcag gctgcctgcc ttcttgccct gtgagctcca gccccacggc 120  
 ctggtgaact gcaactggct ctctctgaag tccgtgcccc acttctcggc ggcagcggcc 180  
 cgggccaacg tcaccagcct ctcttactc tccaaccgca tccaccacct gcacgactcc 240  
 gacttcgtcc acctgtccag cctacgaact ctcaacctca agtggaactg cccgccggct 300  
 ggctcagcc catgcactt cccctgccac atgaccatcg agcccaacac ctctctggcc 360  
 gtgcccaccc tggaggagct gaacctgagc tacaacagca tcacgaccgt gcctgcctg 420  
 cccgactccc tcgtgtccct gtctgtgagc cgcaccaaca tcctgggtgct agacccccacc 480  
 cacctcactg gcctacatgc cctgcgtac ctgtacatgg atggcaactg ctactacaag 540  
 aaccctgcc agggggcgct ggaggtggtg ccgggtgccc tcctcggcct gggcaacctc 600  
 acacatctct cactcaagta caacaatctc acggaggtgc cccgcagcct gccccccagc 660  
 ctggagaccc tgctgttgtc ctacaaccac attgtcacc tgacgcctga ggacctggcc 720  
 aatctgactg ccctgcgcgt gcttgatgtg ggggggaact gccgccgtg tgacctgcc 780  
 cgcaaccct gcagggagtg ccaaaggac caccccaagc tgactctga caccttcagc 840  
 cacctgagcc gcctogaagg cctggtgttg aaagacagtt ctctctacaa cctggacacc 900  
 aggtggttcc gaggcctgga caggctccaa gtgctggacc tgagtgagaa ctctctctac 960  
 gactgcatca ccaagaccac ggccttcag ggcctggccc gactgcgcag cctcaacctg 1020  
 tccttcaatt accacaagaa ggtgtccttt gccacactgc acctggcacc ctctttggg 1080  
 cacctccggc ccctgaagga gctggacatg catggcatct tcttcgctc gctcagtga 1140  
 accacgctcc aacctctggc ccaactgcct atgtccaga ccctgcgcct gcagatgaac 1200  
 ttcattaacc aggccagct cagcatcttt ggggccttcc ctggcctgct gtacgtggac 1260  
 ctatcgaca accgcatcag cggagctgca aggccagtgg ccattactag ggaggtggat 1320  
 ggtagggaga gggctctggc gccttcagg aacctcgctc cactccact ggacactctc 1380  
 cgctcagagg acttcatgcc aaactgcaag gccttcagct tcaccttga cctgtctcg 1440  
 aacaacctgg tgacaatcca gtggagatg ttgtctcgcc tctcagcct cgagtgcctg 1500

cgcctgagcc acaacagcat ctcccaggcg gtcaatggct ctcaagttgt gccgctgacc 1560  
 agcctgcggg tgctggacct gtcccacaac aagctggacc tgtatcacgg gcgctcgttc 1620  
 acggagctgc cgcgcctgga agcactggac ctcaagctaca atagccagcc ctttaccatg 1680  
 caggggtgtgg gccacaacct cagcttcgtg gccagctgc ccgccctgcg ctacctcagc 1740  
 ctggcgcaca atgacatcca tagccgagtg tcccagcagc tctgtagcgc ctcaactgtgc 1800  
 gccctggact ttagcggcaa cgatctgagc cggatgtggg ctgagggaga cctctatctc 1860  
 cgcttcttcc aaggcctaag aagcctagtc tggctggacc tgtcccagaa ccacctgcac 1920  
 accctcctgc cactgtccct ggacaacctc cccaaaagcc tgaagcatct gcctctccgt 1980  
 gacaataacc tggccttctt caactggagc agcctgacct tcctgcccac gctggaaacc 2040  
 ctggacttgg ctggaaacca gctgaaggcc ctaagcaatg gcagcctgcc atctggcacc 2100  
 cagctgcgga ggctggacct cagtggcaac agcatcggtt ttgtgaacct tggcttcttt 2160  
 gccctggcca agcagttaga agagctcaac ctcaagcgcca atgccctcaa gacagtggag 2220  
 cctcctgggt ttggctcgat ggtgggcaac ctgaaagtcc tagacgtgag cgccaaccct 2280  
 ctgcaactgt cctgtggggc gaccttcgtg ggcttctctg tggaggtaca ggctgccgtg 2340  
 cctgggctgc ccagccgct caagtgtggc agtccggggc agtccaggg ccatagcatc 2400  
 tttgcgaag acctgcgcct ctgcctggat gagacctct cgtggaactg ttttggc 2457

<210> 9  
 <211> 1029  
 <212> PRT  
 <213> Bos taurus

<400> 9

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
 1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Glu Gly Thr Leu Pro Ala Phe Leu  
 20 25 30

Pro Cys Glu Leu Gln Pro His Gly Gln Val Asp Cys Asn Trp Leu Phe  
 35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
 50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr  
 100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
 115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu  
 130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr  
 145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn  
 165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly  
 180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu  
 210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala  
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro  
 260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg  
 290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr

305	310	315	320
Asp Tyr Ile Thr Lys Thr Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg	325	330	335
Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His	340	345	350
Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu	355	360	365
Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln	370	375	380
Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn	385	390	395
Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu	405	410	415
Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro	420	425	430
Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu	435	440	445
Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp	450	455	460
Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn	465	470	475
Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu	485	490	495
Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly	500	505	510
Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His	515	520	525
Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln	530	535	540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln  
 545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg  
 565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys  
 580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu  
 595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly  
 610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr  
 625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu  
 645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
 660 665 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu  
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val  
 705 710 715 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 725 730 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile  
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 755 760 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg  
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
 805 810 815

Phe Gly Leu Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met  
 820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys  
 835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu  
 850 855 860

Leu Tyr Asp Ala Val Val Val Phe Asp Lys Val Gln Ser Ala Val Ala  
 865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly  
 885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly  
 900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys  
 915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg  
 930 935 940

Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp  
 945 950 955 960

Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr  
 965 970 975

Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro  
 980 985 990

His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Ile Ala  
 995 1000 1005

Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg  
 1010 1015 1020

Gly Pro Thr Thr Ala Glu  
1025

<210> 10  
<211> 818  
<212> PRT  
<213> Bos taurus  
  
<400> 10

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Glu Gly Thr Leu Pro Ala Phe Leu  
20 25 30

Pro Cys Glu Leu Gln Pro His Gly Gln Val Asp Cys Asn Trp Leu Phe  
35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr  
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu  
130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr  
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn  
165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly  
180 185 190



Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu  
 210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala  
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro  
 260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg  
 290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320

Asp Tyr Ile Thr Lys Thr Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg  
 325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln  
 370 375 380

Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu  
 405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro

420	425	430
Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu		
435	440	445
Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp		
450	455	460
Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn		
465	470	475
Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu		
485	490	495
Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly		
500	505	510
Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His		
515	520	525
Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln		
530	535	540
Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln		
545	550	555
Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg		
565	570	575
Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys		
580	585	590
Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu		
595	600	605
Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly		
610	615	620
Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr		
625	630	635
Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu		
645	650	655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
 660 665 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu  
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val  
 705 710 715 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 725 730 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile  
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 755 760 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg  
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
 805 810 815

Phe Gly

<210> 11

<211> 3191

<212> DNA

<213> Bos taurus

<400> 11

gggaagtggg cgccaagcat ccttcctgc agctgcctcc caacctgccc gccagacct	60
ctggagaagc cgcattccct gtcattggcc cctactgtgc cccgcacccc cttctctctc	120
tgggtgcaggc ggccggcactg gcagcggccc tggccgaggg caccctgcct gccttctgc	180
cctgtgagct ccagcccat ggtcaggtgg actgcaactg gctgttctctg aagtctgtgc	240
cgcacttttc ggctggagcc ccccgggcca atgtcaccag cctctcctta atctccaacc	300

gcatccacca cttgcatgac tctgacttcg tccacctgtc caacctgcgg gtcctcaacc 360  
 tcaagtggaa ctgcccgcg gccggcctca gcccacatgca cttcccctgc cgtatgacca 420  
 tcgagcccaa caccttcctg gctgtgcca cctggagga gctgaacctg agctacaacg 480  
 gcatcacgac cgtgcctgcc ctgcccagtt cctcgtgtc cctgtcgctg agccacacca 540  
 gcatcctggg gctaggcccc acccaactca cgggcctgca cgccctgcgc tttctgtaca 600  
 tggacggcaa ctgctactac atgaaccct gccgcgggc cctggagggtg gcccaggcg 660  
 cctcctcg gctgggcaac ctacgcacc tgtcgctcaa gtacaacaac ctacaggagg 720  
 tgccccgcg cctgcccccc agcctggaca cctgctgct gtcctacaac cacattgtca 780  
 cctggcacc cgaggacctg gccaacctga ctgccctgcg cgtgcttgac gtgggtggga 840  
 actgccgcg ctgcgaccat gccgcgaacc cctgcaggga gtgcccagg aacttcccc 900  
 agctgcacc tgacaccttc agtcacctga gccgcctcga aggcctgggtg ttgaaggaca 960  
 gttctctcta caaactagag aaagattggg tccgcggcct gggcaggctc caagtgtcg 1020  
 acctgagtga gaacttcctc tatgactaca tcaccaagac caccatcttc aacgacctga 1080  
 ccagctgcg cagactcaac ctgtccttca attaccacaa gaagggtgcc ttcgcccacc 1140  
 tgcacctagc gtctcctttt gggagtctgg tgtccctgga gaagctggac atgcacggca 1200  
 tcttcttcg ctccctcacc aacatcacgc tccagtcgct gacccggctg cccaagctcc 1260  
 agagtctgca tctgcagctg aacttcacat accaggccca gctcagcatc tttggggcct 1320  
 tcccagacct gctcttcgtg gacctgtcgg acaaccgcat cagcggagcc gcgacgccag 1380  
 cggccgcctt gggggagggtg gacagcaggg tggaaagtctg gcgattgccc aggggcctcg 1440  
 ctccaggccc gctggacgcc gtcagctcaa aggacttcac gccaaagtgc aacctcaact 1500  
 tcaccttgga cctgtcacgg aacaacctgg tgacaatcca gcaagagatg tttaccgcc 1560  
 tctccgcctt ccagtgcctg cgcctgagcc acaacagcat ctgcaggcg gttaatggct 1620  
 ccagttcgt gccgctgacc agcctgcgag tgctcgacct gtcccacaac aagctggacc 1680  
 tgtaccatgg gcgctcattc acggagctgc cgcagctgga ggcaactggac ctgagctaca 1740  
 acagccagcc cttcagcatg cagggcgtgg gccacaacct cagcttcgtg gccagctgc 1800  
 cctccctgcg ctacctcagc cttgcgcaca atggcatcca cagccgcgtg tcacagaagc 1860  
 tcagcagcg ctcgttgcg gccctggact tcagcggcaa ctccctgagc cagatgtggg 1920  
 ccgagggaga cctctatctc tgctttttca aaggcttgag gaacctggtc cagctggacc 1980  
 tgtccgagaa ccatctgcac accctcctgc ctgctcacct ggacaacctg cccaagagcc 2040

tgcggcagct gcgtctccgg gacaataacc tggccttctt caactggagc agcctgaccg 2100  
 tcctgccccg gctggaagcc ctggatcttg caggaaacca gctgaaggcc ctgagcaacg 2160  
 gcagcctgcc gcctggcatc eggctccaga agctggacgt gagcagcaac agcatcggct 2220  
 tcgtgatccc cggcttcttc gtccgcgcga ctccggctgat agagcttaac ctccagcgcca 2280  
 atgccctgaa gacagtggat ccctcctggg tccgttcttc agcagggacc ctgaaaatcc 2340  
 tagacgtgag cgccaacccg ctccactgcg cctgcggggc ggcctttgtg gacttcctgc 2400  
 tggagagaca ggaggccgtg cccgggctgt ccaggcgcgt cacatgtggc agtccggggc 2460  
 agtccagggg ccgcagcatc ttcacacagg acctgcgcct ctgcctggat gagaccctct 2520  
 ccttggactg ctttggcctc tccactgctaa tgggtggcgt gggcctggca gtgccatgc 2580  
 tgcaccacct ctgtggctgg gacctctggg actgcttcca cctgtgtctg gccatttgc 2640  
 cccgacggcg gcggcagcgg ggcgaggaca ccctgctcta tgatgccgtc gtggtcttcg 2700  
 acaagggtgca gagtgcagtg gctgattggg tgtacaacga gctccgcgtg cagctggagg 2760  
 agcgcggggg gcgcggggcg ctccgcctct gcctggagga gcgagactgg ctccctggta 2820  
 agacgtctct cgagaacctg tgggcctcgg tctacagcag ccgaagacc atgttcgtgc 2880  
 tggaccacac ggaccgggtc agcggcctcc tgcgcgccag ctctctgctg gccagcagc 2940  
 gcctgttggg ggaccgcaag gacgtcgtag tgetggtgat cctgcgcccc gccgcctatc 3000  
 ggtcccgtca cgtgcggctg cgcagcgc ccctgcgcga gacgtcctc ctctggcccc 3060  
 accagcccag tggccagggt agtttctggg ccaacctggg catagccctg accagggaca 3120  
 accgtcactt ctataaccgg aacttctgcc ggggccccac gacagccgaa tagcacagag 3180  
 tgactgcccc g 3191

&lt;210&gt; 12

&lt;211&gt; 2454

&lt;212&gt; DNA

&lt;213&gt; Bos taurus

&lt;400&gt; 12

atgggcccct actgtgcccc gcacccccct tctctcctgg tgcaggcggc ggcactggca 60  
 ggggccctgg ccgagggcac cctgcctgcc ttctgcct gtgagctcca gcccctggt 120  
 cagggtggact gcaactggct gttcctgaag tctgtgccgc acttttcggc tggagcccc 180  
 cgggccaatg tcaccagcct ctcccttaatc tccaaccgca tccaccactt gcatgactct 240  
 gacttcgtcc acctgtccaa cctgcgggtc ctcaacctca agtggaaactg cccgcggggc 300  
 ggctcagcc ccatgcactt cccctgccgt atgaccatcg agcccaacac ctctctggct 360

gtgcccaccc tggaggagct gaacctgagc tacaacggca tcacgaccgt gcctgccctg 420  
 cccagttccc tcgtgtccct gtcgctgagc cacaccagca tcctggtgct agggcccacc 480  
 cacttcaccg gcctgcacgc cctgcgcttt ctgtacatgg acggcaactg ctactacatg 540  
 aaccctgcc cgcgggccct ggaggtggcc ccaggcgccc tcctcggcct gggcaacctc 600  
 acgcacctgt cgctcaagta caacaacctc acggaggtgc cccgcgcct gccccccagc 660  
 ctggacaccc tgctgctgtc ctacaaccac attgtcacc tggcaccga ggacctggcc 720  
 aacctgactg ccctgcgcgt gcttgacgtg ggtgggaact gccgcgcctg cgaccatgcc 780  
 cgcaaccctt gcagggagtg cccaagaac ttccccaagc tgcacctga caccttcagt 840  
 cacctgagcc gcctcgaagg cctggtgttg aaggacagtt ctctctacaa actagagaaa 900  
 gattggttcc gcggcctggg caggtccaa gtgctcgacc tgagtgagaa cttcctctat 960  
 gactacatca ccaagaccac catcttcaac gacctgacc agctgcgcag actcaacctg 1020  
 tccttcaatt accacaagaa ggtgtccttc gccacctgc acctagcgtc ctctttggg 1080  
 agtctggtgt ccctggagaa gctggacatg cacggcatct tcttcgcctc cctcaccaac 1140  
 atcacgtcc agtcgtgac cgggctgccc aagctccaga gtctgcatct gcagctgaac 1200  
 ttcacaaacc agggccagct cagcatcttt ggggccttcc cgagcctgct cttcgtggac 1260  
 ctgtcggaca accgcatcag cggagccgcg acgccagcgg ccgcctggg ggaggtggac 1320  
 agcaggggtg aagtctggcg attgcccagg ggcctcgctc caggcccgct ggacgccgtc 1380  
 agctcaaagg acttcatgcc aagctgcaac ctcaacttca ccttggacct gtcacggaac 1440  
 aacctggtga caatccagca agagatgttt accgcctct cccgcctcca gtgcctgcgc 1500  
 ctgagccaca acagcatctc gcaggcgggt aatggctccc agttcgtgcc gctgaccagc 1560  
 ctgcgagtgc tcgacctgtc ccacaacaag ctggacctgt accatgggcg ctcattcacg 1620  
 gagctgccgc agctggaggc actggacctc agctacaaca gccagccctt cagcatgcag 1680  
 ggcgtgggcc acaacctcag cttcgtggcc cagctgccct ccctgcgcta cctcagcctt 1740  
 gcgcacaatg gcatccacag ccgcgtgtca cagaagctca gcagcgcctc gttgcgcgcc 1800  
 ctggacttca gcggcaactc cctgagccag atgtgggccc agggagacct ctatctctgc 1860  
 tttttcaaag gcttgaggaa cctggctccag ctggacctgt ccgagaacca tctgcacacc 1920  
 ctctgcctc gtcacctgga caacctgccc aagagcctgc ggcagctgcg tctccgggac 1980  
 aataacctgg ccttcttcaa ctggagcagc ctgaccgtcc tgccccggct ggaagccctg 2040  
 gatctggcag gaaaccagct gaaggccctg agcaacggca gcctgccgcc tggcatccgg 2100  
 ctccagaagc tggacgtgag cagcaacagc atcggtctcg tgatccccgg cttcttcgtc 2160

cgcgcgactc ggctgataga gcttaacctc agcgccaatg ccctgaagac agtggatccc 2220  
 tcctgggttcg gttccttagc agggaccctg aaaatcctag acgtgagcgc caaccgctc 2280  
 cactgcgcct gcggggcggc ctttgtggac ttcctgctgg agagacagga ggccgtgccc 2340  
 gggctgtcca ggcgcgtcac atgtggcagt cggggccagc tccagggccg cagcatcttc 2400  
 acacaggacc tgcgcctctg cctggatgag accctctcct tggactgctt tggc 2454

<210> 13  
 <211> 1031  
 <212> PRT  
 <213> Equus caballus

<400> 13

Met Gly Pro Cys His Gly Ala Leu Gln Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Met Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Pro Phe  
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn  
 50 55 60

Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp  
 65 70 75 80

Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met  
 100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
 130 135 140

Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro  
 145 150 155 160

Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly  
 165 170 175  
 Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro  
 180 185 190  
 Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205  
 Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220  
 Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu  
 225 230 235 240  
 Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255  
 Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe  
 260 265 270  
 Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly  
 275 280 285  
 Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe  
 290 295 300  
 Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320  
 Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335  
 Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350  
 His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365  
 Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu  
 370 375 380  
 Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met  
 385 390 395 400



Asn	Phe	Ile	Asn	Gln	Ala	Gln	Leu	Gly	Ile	Phe	Lys	Asp	Phe	Pro	Gly	
				405					410						415	
Leu	Arg	Tyr	Ile	Asp	Leu	Ser	Asp	Asn	Arg	Ile	Ser	Gly	Ala	Val	Glu	
			420					425					430			
Pro	Val	Ala	Thr	Thr	Gly	Glu	Val	Asp	Gly	Gly	Lys	Lys	Val	Trp	Leu	
		435					440					445				
Thr	Ser	Arg	Asp	Leu	Thr	Pro	Gly	Pro	Leu	Asp	Thr	Pro	Ser	Ser	Glu	
	450					455					460					
Asp	Phe	Met	Pro	Ser	Cys	Lys	Asn	Leu	Ser	Phe	Thr	Leu	Asp	Leu	Ser	
465					470					475					480	
Arg	Asn	Asn	Leu	Val	Thr	Val	Gln	Pro	Glu	Met	Phe	Ala	Gln	Leu	Ser	
				485					490						495	
Arg	Leu	Gln	Cys	Leu	Arg	Leu	Ser	His	Asn	Ser	Ile	Ser	Gln	Ala	Val	
			500					505					510			
Asn	Gly	Ser	Gln	Phe	Val	Pro	Leu	Thr	Ser	Leu	Gln	Val	Leu	Asp	Leu	
		515					520					525				
Ser	His	Asn	Lys	Leu	Asp	Leu	Tyr	His	Gly	Arg	Ser	Phe	Thr	Glu	Leu	
	530					535					540					
Pro	Arg	Leu	Glu	Ala	Leu	Asp	Leu	Ser	Tyr	Asn	Ser	Gln	Pro	Phe	Ser	
545					550					555					560	
Met	Arg	Gly	Val	Gly	His	Asn	Leu	Ser	Phe	Val	Ala	Gln	Leu	Pro	Thr	
				565					570						575	
Leu	Arg	Tyr	Leu	Ser	Leu	Ala	His	Asn	Gly	Ile	His	Ser	Arg	Val	Ser	
			580					585					590			
Gln	Gln	Leu	Cys	Ser	Thr	Ser	Leu	Trp	Ala	Leu	Asp	Phe	Ser	Gly	Asn	
		595					600					605				
Ser	Leu	Ser	Gln	Met	Trp	Ala	Glu	Gly	Asp	Leu	Tyr	Leu	Arg	Phe	Phe	
	610					615					620					
Gln	Gly	Leu	Arg	Ser	Leu	Ile	Arg	Leu	Asp	Leu	Ser	Gln	Asn	Arg	Leu	
625					630				635						640	

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln  
 645 650 655  
 Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser  
 660 665 670  
 Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln  
 675 680 685  
 Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln  
 690 695 700  
 Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe  
 705 710 715 720  
 Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
 725 730 735  
 Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu  
 740 745 750  
 Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
 755 760 765  
 Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu  
 770 775 780  
 Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser  
 785 790 795 800  
 Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp  
 805 810 815  
 Asp Cys Phe Gly Leu Ser Leu Leu Val Val Ala Leu Gly Leu Ala Met  
 820 825 830  
 Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His  
 835 840 845  
 Leu Gly Leu Ala Trp Leu Pro Arg Arg Gly Trp Gln Arg Gly Ala Asp  
 850 855 860  
 Ala Leu Ser Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala

- 40 -

35	40	45
Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn		
50	55	60
Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp		
65	70	75 80
Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp		
85	90	95
Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met		
100	105	110
Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu		
115	120	125
Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser		
130	135	140
Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro		
145	150	155 160
Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly		
165	170	175
Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro		
180	185	190
Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr		
195	200	205
Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr		
210	215	220
Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu		
225	230	235 240
Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg		
245	250	255
Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe		
260	265	270

Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe  
 290 295 300

Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu  
 370 375 380

Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Lys Asp Phe Pro Gly  
 405 410 415

Leu Arg Tyr Ile Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Val Glu  
 420 425 430

Pro Val Ala Thr Thr Gly Glu Val Asp Gly Gly Lys Lys Val Trp Leu  
 435 440 445

Thr Ser Arg Asp Leu Thr Pro Gly Pro Leu Asp Thr Pro Ser Ser Glu  
 450 455 460

Asp Phe Met Pro Ser Cys Lys Asn Leu Ser Phe Thr Leu Asp Leu Ser  
 465 470 475 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser  
 485 490 495

Arg Leu Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val  
 500 505 510

Asn Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Gln Val Leu Asp Leu  
 515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu  
 530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser  
 545 550 555 560

Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Thr  
 565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser  
 580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Trp Ala Leu Asp Phe Ser Gly Asn  
 595 600 605

Ser Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe  
 610 615 620

Gln Gly Leu Arg Ser Leu Ile Arg Leu Asp Leu Ser Gln Asn Arg Leu  
 625 630 635 640

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln  
 645 650 655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser  
 660 665 670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln  
 675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln  
 690 695 700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe  
 705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
 725 730 735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu  
 740 745 750

Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
 755 760 765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu  
 770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser  
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp  
 805 810 815

Asp Cys Phe Gly  
 820

<210> 15  
 <211> 3391  
 <212> DNA  
 <213> Equus caballus

<400> 15  
 ctctgttctc tgagctgttg ccgcgtgaag ggactgcgag cacaaagcat cctcctctgc 60  
 agctgctgcc cagtgtgcca gctggaccct ctggatcatc tcccactccc tgtcatgggc 120  
 ccttgccatg gtgccctgca gccctgtct ctctctgtgc aggcggccat gctggccgtg 180  
 gctctggccc aaggcaccct gcctcccttc ctgccctgtg agctccagcc ccacggcctg 240  
 gtgaactgca actggctgtt cctgaagtcc gtgccccact tctcagcagc agcacccegg 300  
 gacaatgtca ccagcctttc cttgctctcc aaccgcatcc accacctcca cgactccgac 360  
 tttgcccac tgtccaacct gcagaaaactc aacctcaaat ggaactgccc gccagccggc 420  
 ctcagcccca tgcaactccc ctgccacatg accatcgagc ccaacacttt cctggctgta 480  
 cccaccctgg aggagctgaa cctgagctac aacggcatca cgactgtgcc tgccctgccc 540  
 agctccctcg tgtccctgat cctgagccgc accaaccatcc tgcagctaga cccaccagc 600  
 ctcacggggc tgcattgccc gcgcttccta tacatggatg gcaactgcta ctacaagaac 660  
 ccctgcgggc gggccctgga ggtggcccca ggcgcctcc ttggcctggg caacctcacc 720  
 cacctgtcac tcaagtacaa caacctcaca acggtgcccc gcagcctgcc ccctagcctg 780  
 gactacctgc tgttgtccta caaccacatt gtcaccctgg cacctgagga cctggccaat 840  
 ctgactgccc tgcgtgtgct cgatgtgggt ggaaactgcc gccgctgtga ccatgcacgc 900  
 aaccctgcg tggagtgccc acataaatcc cccagctgc actccgacac cttcagccac 960

ctaagccgcc tagaaggcct cgtgttgaag gatagttctc tctaccagct gaaccccaga	1020
tgggtccgtg gcctgggcaa cctcacagtg ctcgacctga gtgagaactt cctctacgac	1080
tgcataccca aaaccaaggc attccagggc ctggcccagc tgcgaagact caacttgttc	1140
ttcaattacc ataagaaggt gtccttcgcc cacctgacgc tggcaccctc cttcgggagc	1200
ctgctctccc tgcaggaact ggacatgcat ggcatcttct tccgctcact cagccagaag	1260
acgctccagc cactggcccg cctgcccattg ctccagcgtc tgtatctgca gatgaacttc	1320
atcaaccagg cccagctcgg catcttcaag gacttccttg gtctgcgcta catagacctg	1380
tcagacaacc gcatcagtgg agctgtggag ccggtggcca ccacagggga ggtggatggt	1440
gggaagaagg tctggctgac atccaggagc ctcactccag gccactgga cccccccagc	1500
tctgaggact tcatgccaaag ctgcaagaac ctcagcttca ccttggacct gtcacggaac	1560
aacctggtaa cagtccagcc agagatgttt gccagctct cgcgcctcca gtgcctgcgc	1620
ctgagccaca acagcatctc gcaggcggtc aatggctcac agttcgtgcc actgaccagc	1680
ctgcagggtgc tggacctgtc ccataacaaa ctggacctgt accatgggag ctcgtttacg	1740
gagctgccgc gactggaggc cctggacctc agctacaaca gccagccctt cagcatgcgg	1800
ggtgtggggc acaacctcag ctttgtggcc cagctgcca ccctgcgcta cctcagcctg	1860
gcacacaatg gcatccacag ccgtgtgtcc cagcagctct gcagcacctc gctgtggggc	1920
ctggacttca gcggcaattc cctgagccag atgtgggctg agggagacct ctatctccgc	1980
ttcttccaag gcctgagaag cctaattccgg ctagacctgt ccagaatcg tctgcatacc	2040
ctcctgccat gcacctggg caacctcccc aagagcttgc agctgctgcg tctccgtaac	2100
aattacctgg ccttcttcaa ttggagcagc ctgacctcc tgcccaacct ggaaaccttg	2160
gacctggctg gaaaccagct gaaggctctg agcaatggca gcctgccttc tggcaccag	2220
ctccagaggc tggacgtcag caggaacagc atcatcttcg tggctccctg cttctttgct	2280
ctggccacga ggctgcgaga gctcaacctc agtgccaacg ccctcaggac agaggagccc	2340
tcctggtttg gtttcctagc aggtccctt gaagtccctg atgtgagcgc caacctctg	2400
cactgcgcct gtggggcagc ctttgtggac ttctgtctgc aggttcaggc tgccgtgcct	2460
ggtctgcca gcgcgtcaa gtgtggcagt ccgggccagc tccagggccg cagcatcttc	2520
gcacaagacc tgcgcctctg cctggacaag tccctctcct gggactgttt tggctctctca	2580
ttgtgtgttg tggccctggg cctggccatg cctatgttgc accacctctg cggctgggac	2640
ctctggtact gcttccacct gggcctggcc tggtgcccc ggcgggggtg gcagcggggc	2700



gcggatgccc tgagctatga tgcctttgtg gtcttcgaca aggcacagag cgcagtggcc 2760  
gactgggtgt acaatgaact gcgggtgcgg ctagaggagc gccgtgggcg cggggcgctc 2820  
cgctgtgtc tggaggagcg tgactggcta cctggcaaga cgctgttcga aaacctgtgg 2880  
gcctcagtct acagcagccg caagatgctg tttgtgctgg cccacacgga ccaggtcagt 2940  
ggcctcttgc gtgccagctt cctgctggcc cagcagcgtc tgctggagga ccgcaaggac 3000  
gttgtggtgc tggtaatcct gagccctgac gcccgcggtt cccgttacgt ggggctgcgc 3060  
cagcgcctct gccgccagag tgtcctcttc tggccccacc agcctagtgg ccagcgcagc 3120  
ttctggggcc agctaggcat ggccctgacc agggacaacc gccacttcta taaccagaac 3180  
ttctgccggg gcccgacgat ggctgagtag cacagagtga cagcctggca tgtacaacct 3240  
ccagccctga ccttgccctc ctgcctatga tgcccagtct gcctcactct gtgacgcccc 3300  
tgctctgcct ccgccacct caccctggc atacagcagg cactcaataa atgccactgg 3360  
caggccaaac agccaaaaa aaaaaaaaaa a 3391

<210> 16  
<211> 2460  
<212> DNA  
<213> Equus caballus

<400> 16  
atggggccctt gccatggtgc cctgcagccc ctgtctctcc tgggtgcaggc ggccatgctg 60  
gccgtggctc tggcccaagg caccctgcct ccttctctgc cctgtgagct ccagcccccac 120  
ggcctggtga actgcaactg gctgttcctg aagtccgtgc cccacttctc agcagcagca 180  
ccccgggaca atgtcaccag cctttccttg ctctccaacc gcatccacca cctccacgac 240  
tccgactttg cccaactgtc caacctgcag aaactcaacc tcaaattgaa ctgcccgcc 300  
gccggcctca gcccctgca cttcccctgc cacatgacca tcgagcccaa cactttcctg 360  
gctgtacca cctggagga gctgaacctg agctacaacg gcatcacgac tgtgcctgcc 420  
ctgcccagct cctcgtgtc cctgatcctg agccgcacca acatcctgca gctagacccc 480  
accagcctca cgggcctgca tgccctgcgc ttcctataca tggatggcaa ctgetactac 540  
aagaacccct gcgggcgggc cctggagggtg gcccagcg ccctccttgg cctgggcaac 600  
ctcaccacc tgctactcaa gtacaacaac ctcaaacgg tgccccgag cctgccccct 660  
agcctggagt acctgctgtt gtcctacaac cacattgtca ccctggcacc tgaggacctg 720  
gccaatctga ctgccctgcg tgtgtctgat gtgggtggaa actgccgcg ctgtgaccat 780  
gcacgcaacc cctgcgtgga gtgccacat aaattcccc agctgcactc cgacaccttc 840

agccacctaa gccgcctaga aggcctcgtg ttgaaggata gttctctcta ccagctgaac 900  
 cccagatggt tccgtggcct gggcaacctc acagtgtcg acctgagtga gaacttcctc 960  
 tacgactgca tcacaaaaac caaggcattc cagggcctgg cccagctgcg aagactcaac 1020  
 ttgtccttca attaccataa gaaggtgtcc ttcgcccacc tgacgtggc accctccttc 1080  
 gggagcctgc tctccctgca ggaactggac atgcatggca tcttcttccg ctcaactcagc 1140  
 cagaagacgc tccagccact ggcccgcctg cccatgtcc agcgtctgta tctgcagatg 1200  
 aacttcatca accaggccca gctcggcatc ttcaaggact tccctggtct gcgctacata 1260  
 gacctgtcag acaaccgcat cagtggagct gtggagccgg tggccaccac aggggaggtg 1320  
 gatggtggga agaaggtctg gctgacatcc agggacctca ctccaggccc actggacacc 1380  
 cccagctctg aggacttcat gccaagctgc aagaacctca gcttcacctt ggacctgtca 1440  
 cggaacaacc tggttaacagt ccagccagag atgtttgccc agctctcgcg cctccagtgc 1500  
 ctgcgctga gccacaacag catctcgcag gcggtcaatg gctcacagtt cgtgccactg 1560  
 accagcctgc aggtgtctga cctgtcccat acaaaactgg acctgtacca tgggcgctcg 1620  
 tttacggagc tgccgcgact ggaggccctg gacctcagct acaacagcca gcccttcagc 1680  
 atgcgggggtg tgggccacaa cctcagcttt gtggcccagc tgcccaccct gcgctacctc 1740  
 agcctggcac acaatggcat ccacagccgt gtgtcccagc agctctgcag cacctcgtcg 1800  
 tgggccctgg acttcagcgg caattccctg agccagatgt gggctgaggg agacctctat 1860  
 ctccgcttct tccaaggcct gagaagccta atccggctag acctgtcca gaatcgtctg 1920  
 cataccctcc tgccatgcac cctgggcaac ctcccaga gcttgcagct gctgcgtctc 1980  
 cgtaacaatt acctggcctt cttcaattgg agcagcctga ccctcctgcc caacctggaa 2040  
 accctggacc tggctggaaa ccagctgaag gctctgagca atggcagcct gccttctggc 2100  
 acccagctcc agaggctgga cgtcagcagg aacagcatca tcttcgtggc ccctggcttc 2160  
 tttgctctgg ccacgaggct gcgagagctc aacctcagt ccaacgccct caggacagag 2220  
 gagccctcct ggtttggttt cctagcaggc tccctgaag tcctagatgt gagcgccaac 2280  
 cctctgcact gcgcctgtgg ggcagccttt gtggacttcc tgctgcaggt tcaggctgcc 2340  
 gtgcctggtc tgcccagccg cgtcaagtgt ggcagtccgg gccagctcca gggccgcagc 2400  
 atcttcgcac aagacctgcg cctctgcctg gacaagtccc tctcctggga ctgttttggc 2460

&lt;210&gt; 17

&lt;211&gt; 1029

&lt;212&gt; PRT

&lt;213&gt; Ovis aries

&lt;400&gt; 17

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
 1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu  
 20 25 30

Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe  
 35 40 45

Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
 50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr  
 100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
 115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu  
 130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr  
 145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn  
 165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly  
 180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu  
 210 215 220

Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala  
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro  
 260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg  
 290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320

Asp Tyr Ile Thr Lys Thr Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg  
 325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg  
 370 375 380

Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu  
 405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430

Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp  
 435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp  
 450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn  
465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu  
485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly  
500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr  
515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln  
530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln  
545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg  
565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys  
580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu  
595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly  
610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr  
625                      630                      635                      640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu  
645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu  
690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val  
 705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile  
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg  
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
 805 810 815

Phe Gly Phe Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met  
 820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys  
 835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu  
 850 855 860

Leu Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val Ala  
 865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly  
 885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly  
 900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys  
 915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg

930                                      935                                      940  
 Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp  
 945                                      950                                      955                                      960  
 Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr  
                                     965                                      970                                      975  
 Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro  
                                     980                                      985                                      990  
 His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Met Ala  
                                     995                                      1000                                      1005  
 Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg  
                                     1010                                      1015                                      1020  
 Gly Pro Thr Thr Ala Glu  
                                     1025  
  
 <210> 18  
 <211> 818  
 <212> PRT  
 <213> Ovis aries  
  
 <400> 18  
 Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
 1                                      5                                      10                                      15  
 Ala Ala Leu Ala Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu  
                                     20                                      25                                      30  
 Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe  
                                     35                                      40                                      45  
 Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
                                     50                                      55                                      60  
 Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
 65                                      70                                      75                                      80  
 Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
                                     85                                      90                                      95  
 Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr

100	105	110
Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn		
115	120	125
Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu		
130	135	140
Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr		
145	150	155
His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn		
165	170	175
Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly		
180	185	190
Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn		
195	200	205
Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu		
210	215	220
Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala		
225	230	235
Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg		
245	250	255
Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro		
260	265	270
Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu		
275	280	285
Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg		
290	295	300
Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr		
305	310	315
Asp Tyr Ile Thr Lys Thr Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg		
325	330	335



Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg  
 370 375 380

Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu  
 405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430

Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp  
 435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp  
 450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn  
 465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu  
 485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly  
 500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr  
 515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln  
 530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln  
 545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg  
 565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys  
 580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu  
 595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly  
 610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr  
 625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu  
 645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
 660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu  
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val  
 705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile  
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg  
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
 805 810 815

Phe Gly

&lt;210&gt; 19

&lt;211&gt; 3199

&lt;212&gt; DNA

<213> *Ovis aries*

&lt;400&gt; 19

```

gtcggcacgg gaagtgagcg ccaagcatcc ttccctgcag ctgccgcca acttgcccgc      60
cagaccctct ggagaagccg cattccctgc catgggcccc tactgtgccc cgcaccccct      120
ttctctcttg gtgcaggcgg cggcgtggc agcagccctg gccagggca ccctgcctgc      180
cttctgccc tgtgagctcc agccccggg taaggtgaac tgcaactggc tgttctgaa      240
gtctgtgccc cgcttttcgg cggagcccc cggggccaat gtcaccagcc tctccttaat      300
ctccaaccgc atccaccact tgcacgactc tgacttcgtc cacctgtcca acctgcggggt      360
cctcaacctc aagtggaact gcccgccggc cggcctcagc cccatgcact tcccctgccc      420
catgaccatc gagcccaaca ctttctggc tgtgcccacc ctggaggagc tgaacctgag      480
ctacaatggc atcacgaccg tgcctgccct gccagttct ctcgatccc tgcgtgag      540
ccgaccagc atcctgggtg taggccccac ccacttcacc ggctgcacg ccctgcgctt      600
tctgtacatg gacggcaact gctactataa gaaccctgc cagcaggccg tggagggtgg      660
cccaggcgcc ctcttggcc tgggcaacct cagcacctg tcgtcaagt acaacaacct      720
cacggagggtg ccccgccgcc tgccccccag cctggacacc ctgctgctgt cctacaacca      780
catcatcacc ctggcacccg aggacctggc caatctgact gccctgcgtg tgcttgatgt      840
gggcgggaac tgccgccgt ggcaccacgc ccgaacccc tgaggggagt gcccagaaga      900
cttccccaag ctgcacctg acaccttcag ccacctgagc cgcctcgaag gcctggtgtt      960
gaaggacagt tctctctaca aactagagaa agactggttc cgcggcctgg gcagggtcca     1020
agtgtctgac ctgagtgaga acttcctcta tgactacatc accaagacca ccatcttcag     1080
gaacctgacc cagctgcgca gactcaacct gtccctcaat taccacaaga aggtgtcctt     1140
cgccacctg caactggcac cctcctttgg gggcctgggt tccctggaga agctggacat     1200
gcacggcatc ttcttccgct ccctcaccaa caccacgtc cggccgctga cccagctgcc     1260
caagctccag agtctgagtc tgcagctgaa cttcatcaac caggccgagc tcagcatctt     1320
tggggccttc ccgagcctgc tcttcgtgga cctgtcggac aaccgcatca gcggagctgc     1380
gaggccggtg gccgccctcg gggagggtgga cagcggggtg gaagtctggc ggtggcccag     1440

```

gggcctcgct ccaggcccg c tggccgccgt cagcgcaaag gacttcatgc caagctgcaa 1500  
 cctcaacttc accttggacc tgtcacggaa caacctgggtg acgatccagc aggagatggt 1560  
 taccgccttc tcccgctcc agtgcccg cctgagccac aacagcatct cgcaggcggt 1620  
 taatggctcg cagttcgtgc cgctgacccg cctgcgagtg ctgcacctgt cctacaacaa 1680  
 gctggacctg taccatgggc gctcggtcac ggagctgccg cagctggagg cactggacct 1740  
 cagctacaac agccagccct tcagcatgca gggcggtggc cacaacctca gcttcgtggc 1800  
 ccagctgccg tcctcgct acctcagcct tgcgcacaac ggcatccaca gccgcgtgtc 1860  
 acagaagctc agcagcgct cgctgcgcgc cctggacttc agcggcaact ccctgagcca 1920  
 gatgtgggcc gagggagacc tctatctctg cttcttcaaa ggcttgagga acctggtcca 1980  
 gctggacctg tccaagaacc acctgcacac cctcctgcct cgtcacctgg ataacctgcc 2040  
 caagagcctg cggcagctgc gtctccggga caataacctg gccttcttca actggagcag 2100  
 cctgactgtt ctgccccagc tgggaagccct ggatctggcg ggaaaccagc tgaaggccct 2160  
 gagcaacggc agcctgccac ctggcaccgc gctccagaag ctggacgtga gcagcaacag 2220  
 catcggttt gtgaccctg gcttctttgt ccttgccaac cggtgaaag agcttaacct 2280  
 cagcgccaac gccctgaaga cagtggatcc cttctgggtc ggtcgcttaa cagagacct 2340  
 gaatatccta gacgtgagcg ccaaccgcct cactgtgcc tgcggggcg cctttgtgga 2400  
 ctctctgtg gagatgcagg cggccgtgcc tgggctgtcc aggcgcgtca cgtgtggcag 2460  
 tccgggccag ctccagggcc gcagcatctt cgcacaggac ctgcgcctct gcctggatga 2520  
 gaccctctcc ttggactgct ttggcttctc gctgctaag gtggcgctgg gcctggcggt 2580  
 gcccatgctg caccacctct gtggctggga cctgtggtac tgcttccacc tgtgtctggc 2640  
 ccatttgccc cgacggcggc ggcagcggg cgaggacacc ctgctctacg atgcctcgt 2700  
 ggtcttcgac aaggcgcaga gtgcagtggc cgactgggtg tacaacgagc tccgcgtgca 2760  
 gctggaggag cgcgcgggc gccggcgct ccgcctctgc ctggaggagc gagactggct 2820  
 ccctggcaag acgctcttcg agaacctgtg ggcctcggtc tacagcagcc gtaagaccat 2880  
 gtctgtgtg gaccacacgg accgggtcag tggcctcctg cgcgccagct tcctgctggc 2940  
 ccagcagcgc ctgttgagg accgcaagga tgtcgtggtg ctggtgatcc tgcgccccgc 3000  
 cgcctaccgg tcccgctacg tgcggctgcg ccagcgctc tgccgccaga gcgtcctcct 3060  
 ctggccccac cagcccagtg gccagggtag cttctgggcc aacctgggca tggcctgac 3120  
 cagggacaac cgccacttct ataaccggaa cttctgcccg ggccccacga cagccgaata 3180

gcacagagtg actgcccag

3199

&lt;210&gt; 20

&lt;211&gt; 2454

&lt;212&gt; DNA

&lt;213&gt; Ovis aries

&lt;400&gt; 20

```

atggggccct actgtgcccc gcaccccctt tctctcctgg tgcaggcggc ggcgctggca    60
gcagccctgg ccaggggcac cctgcctgcc ttcttgccct gtgagctcca gccccggggt    120
aaggtgaact gcaactggct gttcctgaag tctgtgccgc gcttttcggc cggagcccc    180
cgggccaatg tcaccagcct ctcttaatc tccaaccgca tccaccactt gcacgactct    240
gacttcgtcc acctgtccaa cctgcgggtc ctcaacctca agtgggaactg cccgccggcc    300
ggcctcagcc ccattgcactt cccctgccgc atgaccatcg agcccaacac ctctctggct    360
gtgcccaccc tggaggagct gaacctgagc tacaatggca tcacgaccgt gcctgccctg    420
cccagttctc tcgtatccct gtcgctgagc cgcaccagca tcttggtgct agggccccacc    480
cacttcaccg gcctgcacgc cctgcgcttt ctgtacatgg acggcaactg ctactataag    540
aaccctgcc agcaggccgt ggagggtggc ccaggcgccc tcttgggcct gggcaacctc    600
acgcacctgt cgctcaagta caacaacctc acggagggtgc cccgccgcct gccccccagc    660
ctggacaccc tgctgctgtc ctacaaccac atcatcacc tggcaccgga ggacctggcc    720
aatctgactg ccctgcgtgt gcttgatgtg ggcgggaact gccgccgctg cgaccacgcc    780
cgcaaccctt gcagggagtg cccaaagaac tccccaaagc tgcaccctga caccttcagc    840
cacctgagcc gcctcgaagg cctgggtgtg aaggacagtt ctctctacaa actagagaaa    900
gactgggtcc ggggcctggg caggctccaa gtgctcgacc tgagtgagaa cttcctctat    960
gactacatca ccaagaccac catcttcagg aacctgacct agctgcgcag actcaacctg   1020
tccttcaatt accacaagaa ggtgtccttc gccacctgc aactggcacc ctctttggg   1080
ggcctggtgt ccctggagaa gctggacatg cacggcatct tcttcgctc cctcaccaac   1140
accacgtccc ggccgctgac ccagctgccc aagctccaga gtctgagtct gcagctgaac   1200
ttcatcaacc aggccgagct cagcatcttt ggggccttcc cgagcctgct ctctgtggac   1260
ctgtcggaca accgcatcag cggagctgcg aggcgggtgg ccgccctcgg ggaggtggac   1320
agcgggggtg aagtctggcg gtggcccagg ggcctcgctc caggcccgct ggccgccgtc   1380
agcgcaaagg acttcatgcc aagctgcaac ctcaacttca ccttggacct gtcacggaac   1440
aacctggtga cgatccagca ggagatgttt acccgctctt cccgcctcca gtgcctgcgc   1500

```

ctgagccaca acagcatctc gcaggcggtt aatggctcgc agttcgtgcc gctgacccgc 1560  
 ctgcgagtgc tcgacctgtc ctacaacaag ctggacctgt accatgggcg ctcgttcacg 1620  
 gagctgccgc agctggaggc actggacctc agctacaaca gccagccctt cagcatgcag 1680  
 ggcgtggggc acaacctcag cttcgtggcc cagctgccgt ccctgcgcta cctcagcctt 1740  
 gcgcacaacg gcatccacag ccgcgtgtca cagaagctca gcagcgctc gctgcgcgcc 1800  
 ctggacttca gcggcaactc cctgagccag atgtgggccc agggagacct ctatctctgc 1860  
 ttcttcaaag gcttgaggaa cctggtccag ctggacctgt ccaagaacca cctgcacacc 1920  
 ctctgcctc gtcacctgga taacctgccc aagagcctgc ggcagctgcg tctccgggac 1980  
 aataacctgg ctttcttcaa ctggagcagc ctgactgttc tgccccagct ggaagccctg 2040  
 gatctggcgg gaaaccagct gaaggccctg agcaacggca gcctgccacc tggcaccggg 2100  
 ctccagaagc tggacgtgag cagcaacagc atcggtttg tgaccttggt cttctttgtc 2160  
 cttgccaaac ggctgaaaga gcttaacctc agcgccaacg ccctgaagac agtggatccc 2220  
 ttctggttcg gtcgcttaac agagaccctg aatatcctag acgtgagcgc caaccgctc 2280  
 cactgtgcct gcggggcggc ctttgtggac ttctgtctgg agatgcaggc ggccgtgcct 2340  
 gggctgtcca ggcgcgtcac gtgtggcagt ccgggccagc tccagggccg cagcatcttc 2400  
 gcacaggacc tgcgcctctg cctggatgag accctctcct tggactgctt tggc 2454

<210> 21

<211> 1032

<212> PRT

<213> Canis familiaris

<400> 21

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
1 5 10 15

Ala Ala Ala Leu Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Pro Arg Gly Asn  
50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
65 70 75 80

Tyr Asp Phe Val His Phe Val His Leu Arg Arg Leu Asn Leu Lys Trp  
                                     85                                    90                                    95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met  
                                     100                                    105                                    110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Asp Leu  
                                     115                                    120                                    125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
                                     130                                    135                                    140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro  
                                     145                                    150                                    155                                    160

Ala Thr Leu Ala Gly Leu Tyr Ala Leu Arg Phe Leu Phe Leu Asp Gly  
                                     165                                    170                                    175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Leu Gln Val Ala Pro  
                                     180                                    185                                    190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
                                     195                                    200                                    205

Asn Asn Leu Thr Val Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr  
                                     210                                    215                                    220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu  
                                     225                                    230                                    235                                    240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
                                     245                                    250                                    255

Arg Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Gly Phe  
                                     260                                    265                                    270

Pro Gln Leu His Pro Asn Thr Phe Gly His Leu Ser His Leu Glu Gly  
                                     275                                    280                                    285

Leu Val Leu Arg Asp Ser Ser Leu Tyr Ser Leu Asp Pro Arg Trp Phe  
                                     290                                    295                                    300

His Gly Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu  
                                     305                                    310                                    315                                    320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu  
 370 375 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu  
 385 390 395 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu  
 420 425 430

Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val  
 435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly  
 450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp  
 465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg  
 485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln  
 500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu  
 515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr  
 530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro



[illegible]

Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly  
 785 790 795 800

Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu  
 805 810 815

Ser Trp Val Cys Phe Ser Leu Ser Leu Leu Ala Val Ala Leu Ser Leu  
 820 825 830

Ala Val Pro Met Leu His Gln Leu Cys Gly Trp Asp Leu Trp Tyr Cys  
 835 840 845

Phe His Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Arg Gly  
 850 855 860

Val Asp Ala Leu Ala Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln  
 865 870 875 880

Ser Ser Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu  
 885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp  
 900 905 910

Trp Val Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr  
 915 920 925

Ser Ser Arg Lys Thr Leu Phe Val Leu Ala Arg Thr Asp Arg Val Ser  
 930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Cys Pro Asp Ala His  
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
 980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln  
 995 1000 1005

Leu Gly Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln  
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Thr Ala  
1025 1030

<210> 22  
<211> 822  
<212> PRT  
<213> Canis familiaris

<400> 22

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
1 5 10 15

Ala Ala Ala Leu Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Pro Arg Gly Asn  
50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
65 70 75 80

Tyr Asp Phe Val His Phe Val His Leu Arg Arg Leu Asn Leu Lys Trp  
85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met  
100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Asp Leu  
115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro  
145 150 155 160

Ala Thr Leu Ala Gly Leu Tyr Ala Leu Arg Phe Leu Phe Leu Asp Gly  
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Leu Gln Val Ala Pro  
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Val Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Gly Phe  
 260 265 270

Pro Gln Leu His Pro Asn Thr Phe Gly His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Arg Asp Ser Ser Leu Tyr Ser Leu Asp Pro Arg Trp Phe  
 290 295 300

His Gly Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu  
 370 375 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu  
 385 390 395 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu  
 420 425 430

Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val  
 435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly  
 450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp  
 465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg  
 485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln  
 500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu  
 515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr  
 530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro  
 545 550 555 560

Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu  
 565 570 575

Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg  
 580 585 590

Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser  
 595 600 605

Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg  
 610 615 620

Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn  
 625 630 635 640

Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser  
 645 650 655

Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp

660	665	670
Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly		
675	680	685
Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln		
690	695	700
Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro		
705	710	715
Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala		
725	730	735
Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly		
740	745	750
Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys		
755	760	765
Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro		
770	775	780
Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly		
785	790	795
Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu		
805	810	815
Ser Trp Val Cys Phe Ser		
820		

<210> 23  
 <211> 3334  
 <212> DNA  
 <213> Canis familiaris

<400> 23	
aggaaggggc tgtgagctcc aagcatcctt tcctgcagct gctgcccagc ctgccagcca	60
gaccctctgg agaagcccc gtcacctgtc atgggcccct gccgtggcgc cctgcacccc	120
ctgtctctcc tgggtgcaggc tgccgcgcta gccctggccc tggccaggg caccctgcct	180
gccttcctgc cctgtgagct ccagcccat ggctgggtga actgcaactg gctgttcctc	240
aagtccgtgc cccgcttctc ggcagctgca ccccgcggtg acgtcaccag cctttccttg	300

tactccaacc gcatccacca cctccatgac tatgactttg tccacttcgt ccacctgcgg	360
cgtctcaatc tcaagtggaa ctgcccggcc gccagcctca gcccacatgca ctttcctgt	420
cacatgacca ttgagcccaa caccttcctg gctgtgcca ccctagagga cctgaatctg	480
agctataaca gcatcacgac tgtgcccggc ctgccagtt cgcttggtgc cctgtccctg	540
agccgcacca acatcctggt gctggaccct gccaccctgg caggccttta tgcctgcgc	600
ttcctgttcc tggatggcaa ctgctactac aagaaccct gccagcaggc cctgcagggt	660
gcccagggtg ccctcctggg cctgggcaac ctcacacacc tgtcactcaa gtacaacaac	720
ctcacctggg tgccgcgggg cctgcccccc agcctggagt acctgctctt gtccataaac	780
cacatcatca ccctggcacc tgaggacctg gccaatctga ctgccctgcg tgtcctcgat	840
gtgggtggga actgtcgccg ctgtgacct gcccgtaacc cctgcaggga gtgcccgaag	900
ggcttcccc agctgcaccc caacaccttc ggccacctga gccacctga aggcctggtg	960
ttgagggaca gctctctcta cagcctggac ccaggtggt tccatggcct gggcaacctc	1020
atggtgctgg acctgagtga gaacttcctg tatgactgca tcacaaaac caaagccttc	1080
tacggcctgg ccggtctgcg cagactcaac ctgtccttca attatcataa gaagggtgcc	1140
tttgcccacc tgcactctggc atcctccttc gggagcctac tgtccctgca ggagctggac	1200
atacatggca tcttcttccg ctgctcagc aagaccagc tccagtcgtt ggcccacctg	1260
cccatgctcc agcgtctgca tctgcagttg aactttatca gccaggccca gctcagcatc	1320
ttcggcgctt tccctggact gcggtacgtg gacttgctag acaaccgcat cagtggagct	1380
gcagagcccg cggctgccac aggggaggta gaggcagact gtggggagag agtctggcca	1440
cagtcccggg accttgctct gggccactg ggcaccccg gctcagaggc cttcatgccg	1500
agctgcagga ccctcaactt caccttggac ctgtctcgga acaacctagt gactgttcag	1560
ccggagatgt ttgtccggct ggcgcgcctc cagtgcctgg gcctgagcca caacagcatc	1620
tcgcaggcgg tcaatggctc gcagttcgtg cctctgagca acctgcgggt gctggacctg	1680
tcccataaca agctggacct gtaccacggg cgctcgttca cggagctgcc gcggtggag	1740
gccttggacc tcagctacaa cagccagccc ttcagcatgc ggggcgtggg ccacaatctc	1800
agctttgtgg cacagctgcc agcctgcgc tacctcagcc tggcgcacaa tggcatccac	1860
agccgcgtgt ccagcagct ccgcagcgcc tcgctccggg ccctggactt cagtggcaat	1920
accctgagcc agatgtgggc cgaggagac ctctatctcc gcttcttcca aggcctgaga	1980
agcctggttc agctggacct gtcccagaat cgctgcata ccctcctgcc acgcaacctg	2040
gacaacctcc ccaagagcct gcggctcctg cggtccgtg acaattacct ggctttcttc	2100

aactggagca gcctggccct cctacccaag ctggaagccc tggacctggc gggaaaccag 2160  
ctgaaggccc tgagcaatgg cagcttgccc aacggcacc agctccagag gctggacctc 2220  
agcggcaaca gcacggcctt cgtgggtccc agcttttttg ccctggccgt gaggcttcga 2280  
gagctcaacc tcagcgccaa cgccctcaag acggtggagc cctcctgggt tggttccctg 2340  
gcggttgccc tgaaagtcc agacgtgacc gccaacccct tgcatcgcc ttgcggcgca 2400  
accttcgtgg acttcttgct ggaggtgcag gctgcggtgc ccggcctgcc tagccgtgtc 2460  
aagtgcggca gcccgggcca gctccagggc cgcagcatct tcgcacagga cctgcgcctc 2520  
tgcctggacg aagcgctctc ctgggtctgt ttcagcctct cgctgctggc tgtggccctg 2580  
agcctggctg tgcccatgct gcaccagctc tgtggctggg acctctggta ctgcttcac 2640  
ctgtgcctgg cctggctgcc ccggcggggg cgggcggggg gtgtggatgc cctggcctat 2700  
gacgccttcg tggctctcga caaggcgag agctcgggtg cggactgggt gtacaatgag 2760  
ctgcgggtac agctagagga gcgccgtggg cgccggggcg tacgcctgtg tctggaggaa 2820  
cgtgactggg taccggcaa aacctcttc gagaacctct gggcctcagt ttacagcagc 2880  
cgcaagacgc tgtttgtgct ggcccgacg gacagagtca gggcctcct cgtgcccagc 2940  
ttcctgctgg cccaacagcg cctgctggag gaccgcaagg acgtcgtggg gctggtgatc 3000  
ctgtgccccg acgcccaccg ctcccgctat gtgcggctgc gccagcgct ctgccgccag 3060  
agtgtcctcc tctggcccca ccagcccagt ggccagcgca gcttctgggc ccagctgggc 3120  
acggccctga ccagggacaa ccgccacttc tacaaccaga acttctgccc gggccccacg 3180  
acagcctgat aggcagacag cccagcacct tcgcgcccct acacctgcc tgtctgtctg 3240  
ggatgcccga cctgctggct ctacaccgcc gctctgtctc ccctacacc agccctggca 3300  
taaagcgacc gctcaataaa tgctgctggg agac 3334

&lt;210&gt; 24

&lt;211&gt; 2466

&lt;212&gt; DNA

&lt;213&gt; Canis familiaris

&lt;400&gt; 24

atgggcccct gccgtggcg cctgcacccc ctgtctctcc tgggtgcaggc tgccgcgcta 60  
gccctggccc tggcccaggg caccctgcct gccttcctgc cctgtgagct ccagcccat 120  
ggcctgggtga actgcaactg gctgttctc aagtccgtgc ccgcttctc ggcagctgca 180  
ccccgcggta acgtcaccag ctttctcttg tactccaacc gcacccacca cctccatgac 240  
tatgactttg tccacttcgt ccacctggg cgtctcaatc tcaagtggaa ctgcccggcc 300



gccagcctca gccccatgca ctttcctgt cacatgacca ttgagcccaa caccttcctg 360  
 gctgtgcca ccctagagga cctgaatctg agctataaca gcatcacgac tgtgcccgcc 420  
 ctgcccagtt cgcttgtgtc cctgtccctg agccgcacca acatcctggg gctggaccct 480  
 gccaccctgg caggccttta tgccctgccc ttctgttcc tggatggcaa ctgctactac 540  
 aagaaccct gccagcaggc cctgcagggt gcccagggt ccctcctggg cctgggcaac 600  
 ctcacacacc tgtcactcaa gtacaacaac ctcaccgtgg tgccgcgggg cctgcccccc 660  
 agcctggagt acctgtctt gtccataaac cacatcatca ccctggcacc tgaggacctg 720  
 gccaatctga ctgcccctgc tgctctgat gtgggtggga actgtcgcg ctgtgaccat 780  
 gcccgtaac cctgcaggga gtgcccgaag ggcttcccc agctgcaccc caacaccttc 840  
 ggccacctga gccacctga aggcctgggt ttgagggaca gctctctcta cagcctggac 900  
 cccagggtgt tccatggcct gggcaacctc atgggtgctg acctgagtga gaacttcctg 960  
 tatgactgca tcacaaaaac caaagccttc tacggcctgg cccggctgcg cagactcaac 1020  
 ctgtccttca attatcataa gaagggtgtc ttgcccacc tgcactggc atcctccttc 1080  
 gggagcctac tgtccctgca ggagctggac atacatggca tcttcttcg ctgctcagc 1140  
 aagaccacgc tccagtcgtt ggcccacctg cccatgtctc agcgtctgca tctgcagttg 1200  
 aactttatca gccaggccca gctcagcatc ttccggcctc tccctggact gcggtacgtg 1260  
 gacttgtcag acaaccgcat cagtggagct gcagagcccg cggctgccac aggggaggta 1320  
 gaggcagact gtggggagag agtctggcca cagtcccggt acctgtctt gggcccactg 1380  
 ggcacccccg gctcagaggc cttcatgccg agctgcagga ccctcaactt caccttgga 1440  
 ctgtctcgga acaacctagt gactgttcag ccggagatgt ttgtccggct ggcgcgctc 1500  
 cagtgcctgg gcctgagcca caacagcatc tcgcaggcgg tcaatggctc gcagttcgtg 1560  
 cctctgagca acctgcgggt gctggacctg tcccataaca agctggacct gtaccacggg 1620  
 cgctcggtca cggagctgcc gcggctggag gccttgacc tcagctacaa cagccagccc 1680  
 ttcagcatgc ggggcgtggg ccacaatctc agctttgtgg cacagctgcc agccctgcgc 1740  
 tacctcagcc tggcgacaaa tggcatccac agccgcgtgt cccagcagct ccgcagcgcc 1800  
 tcgctccggg ccctggactt cagtggcaat accctgagcc agatgtgggc cgaggagac 1860  
 ctctatctcc gcttcttcca aggcctgaga agcctgggtc agctggacct gtcccagaat 1920  
 cgctgcata ccctcctgcc acgcaacctg gacaacctcc ccaagagcct gcggctcctg 1980  
 cggctccgtg acaattacct ggcttcttc aactggagca gcctggccct cctacccaag 2040

ctggaagccc tggacctggc gggaaaccag ctgaaggccc tgagcaatgg cagcttgccc 2100  
 aacggcaccc agctccagag gctggacctc agcggcaaca gcatcggett cgtggtcccc 2160  
 agcttttttg ccctggccgt gaggttcga gagctcaacc tcagcgccaa cgcctcaag 2220  
 acggtggagc cctcctggtt tggttccctg gcgggtgccc tgaaagtcct agacgtgacc 2280  
 gccaacccct tgcattgcgc ttgcggcgca accttcgtgg acttcttgct ggaggtgcag 2340  
 gctgcggtgc ccggcctgcc tagccgtgtc aagtgcggca gcccgggcca gctccagggc 2400  
 cgcagcatct tcgcacagga cctgcgcctc tgcttgacg aagcgctctc ctgggtctgt 2460  
 ttcagc 2466

<210> 25  
 <211> 1031  
 <212> PRT  
 <213> Felis catus

<400> 25

Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Gly Asn  
 50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
 65 70 75 80

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met  
 100 105 110

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
 130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro  
 145 150 155 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe  
 260 265 270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe  
 290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu  
 370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu  
 420 425 430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu  
 435 440 445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu  
 450 455 460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser  
 465 470 475 480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser  
 485 490 495

Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val  
 500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu  
 515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu  
 530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser  
 545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala  
 565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser  
 580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn  
 595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe

610	615	620
Arg Gly Leu Arg Ser Leu Val Arg Leu Asp Leu Ser Gln Asn Arg Leu		
625	630	635 640
His Thr Leu Leu Pro Arg Thr Leu Asp Asn Leu Pro Lys Ser Leu Arg		
	645	650 655
Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser		
	660	665 670
Leu Val Leu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln		
	675	680 685
Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln Leu Gln		
	690	695 700
Arg Leu Asp Leu Ser Ser Asn Ser Ile Ser Phe Val Ala Ser Ser Phe		
	705	710 715 720
Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala		
	725	730 735
Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu		
	740	745 750
Lys Val Leu Asp Val Thr Gly Asn Pro Leu His Cys Ala Cys Gly Ala		
	755	760 765
Ala Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu		
	770	775 780
Pro Gly His Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser		
	785	790 795 800
Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp		
	805	810 815
Asp Cys Phe Gly Leu Ser Leu Leu Thr Val Ala Leu Gly Leu Ala Val		
	820	825 830
Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His		
	835	840 845

Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Gly Ala Asp  
 850 855 860

Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala  
 865 870 875 880

Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg  
 885 890 895

Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu  
 900 905 910

Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser  
 915 920 925

Arg Lys Met Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu  
 930 935 940

Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg  
 945 950 955 960

Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His Arg Ser  
 965 970 975

Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu  
 980 985 990

Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly  
 995 1000 1005

Thr Ala Leu Thr Arg Asp Asn Gln His Phe Tyr Asn Gln Asn Phe  
 1010 1015 1020

Cys Arg Gly Pro Thr Thr Ala Glu  
 1025 1030

<210> 26  
 <211> 820  
 <212> PRT  
 <213> Felis catus

<400> 26

Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Gly Asn  
 50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
 65 70 75 80

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met  
 100 105 110

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
 130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro  
 145 150 155 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe  
 260 265 270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe  
 290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu  
 370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu  
 420 425 430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu  
 435 440 445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu  
 450 455 460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser  
 465 470 475 480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser  
 485 490 495



Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val  
 500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu  
 515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu  
 530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser  
 545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala  
 565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser  
 580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn  
 595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe  
 610 615 620

Arg Gly Leu Arg Ser Leu Val Arg Leu Asp Leu Ser Gln Asn Arg Leu  
 625 630 635 640

His Thr Leu Leu Pro Arg Thr Leu Asp Asn Leu Pro Lys Ser Leu Arg  
 645 650 655

Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser  
 660 665 670

Leu Val Leu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln  
 675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln Leu Gln  
 690 695 700

Arg Leu Asp Leu Ser Ser Asn Ser Ile Ser Phe Val Ala Ser Ser Phe  
 705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala

[illegible]

tcataccacct	ggcacctgag	gacctggcca	acctgaccgc	cctgcgtgtg	ctcgatgtgg	840
gtgggaactg	ccgtcgctgt	gaccacgccc	gcaaccctg	tatggagtgc	cccaagggct	900
tcccgacact	gcaccctgac	accttcagcc	acctgaacca	cctcgaaggc	ctggtgttga	960
aggacagctc	tctctacaac	ctgaacccca	gatggttcca	tgccctgggc	aacctcatgg	1020
tgctggacct	gagtgagaac	ttcctatatg	actgcatcac	caaaaccaca	gccttccagg	1080
gcctggccca	gctgcgcaga	ctcaacttgt	ctttcaatta	ccacaagaag	gtgtcctttg	1140
cccacctgca	tctggcgccc	tccttcggga	gcctgctctc	cctgcagcag	ctggacatgc	1200
atggcatctt	cttcgctcg	ctcagcgaga	ccacgctccg	gtcgtgtgtc	cacctgcca	1260
tgctccagag	tctgcacctg	cagatgaact	tcataatca	ggcccagctc	agcatcttcg	1320
gggccttccc	tggcctgcga	tacgtggacc	tgtagacaa	ccgcataagt	ggagccatgg	1380
agctggcggc	tgccacgggg	gaggtggatg	gtggggagag	agtccggctg	ccatctgggg	1440
acctagctct	gggcccaccg	ggcacccta	gtccgaggg	cttcatgcca	ggctgcaaga	1500
ccctcaactt	caccttgga	ctgtcacgga	acaacctagt	gacaatccag	ccagagatgt	1560
ttgcccggt	ctcgcgctc	cagtgcctgc	tcctgagccg	caacagcatc	tcgaggcag	1620
tcaacggctc	acaatttatg	ccgtgacca	gcctgcaggt	gctggacctg	tcccataaca	1680
agctggacct	gtaccatggg	cgctctttca	cggagctgcc	gcggctggag	gccctggacc	1740
tcagctacaa	cagccagccc	ttcagcatgc	agggcgtagg	tcacaacctc	agctttgtgg	1800
cacagctgcc	ggccctgcgc	tatctcagcc	tggcgacaaa	cgacatccac	agccgtgtgt	1860
cccagcagct	ctgcagcgcc	tcgtgcggg	ccttggaactt	cagcggcaat	gccttgagcc	1920
ggatgtgggc	cgaggagag	ctgtatctcc	acttcttccg	aggcctgagg	agcctggtcc	1980
ggttgatct	gtcccagaat	cgctgcata	ccctcttgcc	acgcacctg	gacaacctcc	2040
ccaagagcct	gcggctgctg	cgtctccgtg	acaattatct	ggctttcttc	aactggagca	2100
gcctggtcct	cctccccagg	ctggaagccc	tggacctggc	gggaaaccag	ctgaaggccc	2160
tgagcaacgg	cagcttgcc	aatggaaccc	agctccagag	gctggacctc	agcagcaaca	2220
gtatcagctt	cgtggcctcc	agcttttttg	ctctggccac	caggctgcga	gagctcaacc	2280
tcagtgccaa	cgcctcaag	acggtggagc	cctcctggtt	cggttctcta	gcgggcaccc	2340
tgaaagtcct	agatgtgact	ggcaaccccc	tgactgcgc	ctgtggggcg	gccttcgtgg	2400
acttcttgct	ggaggtgcag	gctgcagtgc	ccggcctgcc	aggccacgtc	aagtgtggca	2460
gtccaggtca	gctccagggc	cgcagcatct	ttgcgcagga	tctgcgcctc	tgctggatg	2520
agggcctctc	ctgggactgt	tttggcctct	cgctgctgac	cgtggccctg	ggcctggccg	2580

tgcccatgct gcaccacctc tgtggtggg acctctggta ctgcttccac ctgtgcctgg 2640  
 cctggctgcc ccggcggggg cggcggcggg gcgcggatgc cctgccctac gatgcctttg 2700  
 tggctcttca caaggcacag agcgcggtgg ccgactgggt gtacaacgag ctgcgggtac 2760  
 ggctagagga gcgccgtgga cggcgagcgc tccgcctgtg cctggaggaa cgtgactggc 2820  
 taccgcgtaa aacgctcttt gagaacctgt gggcctcagt ttacagcagc cgcaagatgc 2880  
 tgtttgtgct ggcccacaca gacagggtea ggggcctctt gcgcgccagc tttctgctgg 2940  
 cccagcagcg cctgctggag gaccgcaagg acgttgtggg gctggatgc ctgcgccccg 3000  
 acgcccaccg cttccgctat gtgcggctgc gccagcgcct ctgcgccag agcgtcctcc 3060  
 tctggcccca ccagcccagt ggccagcgca gcttctgggc ccagctgggc acggccctga 3120  
 ccagggacaa ccagcacttc tataaccaga acttctgccc gggcccccacg acggcagagt 3180  
 gaccgcccag caccccaagc ctctacacc ttgcctgtct gcctgggatg ccggg 3235

<210> 28

<211> 2460

<212> DNA

<213> *Felis catus*

<400> 28

atggggccct gccatgggc cctgcacccc ctgtctctcc tggatgcaggc tgccgcgctg 60  
 gccgtggccc tggcccaggg caccctgcct gcctttctgc cctgtgagct ccagcgccac 120  
 ggcctgggtga attgcgactg gctgttcctc aagtccgtgc cccacttctc ggccggcagcg 180  
 ccccggtgta acgtcaccag cctttccctg tactccaacc gcatccacca cctccacgac 240  
 tccgactttg tccacctgtc cagcctgcgg cgtctcaacc tcaaattgaa ctgcccaccc 300  
 gccagcctca gcccctatgca ctccccctgt cacatgacca ttgagcccca caccctctctg 360  
 gccgtgcccc ccctggagga gctgaacctg agctacaaca gcatcacgac agtaccgcgc 420  
 ctgcccagtt cctcgtgtc cctgtccttg agcgtacca acatcctggg gctggaccct 480  
 gccaacctcg cagggtgca ctccctgcgc tttctgttcc tggatggcaa ctgtactac 540  
 aagaacccct gccgcaggc cctgcagggt gcccggggcg cctccttgg cctgggcaac 600  
 cttacgcacc tgtcactcaa gtacaacaac ctactgcgg tgccccgcgg cctgcccccc 660  
 agcctggagt acctgctatt gtccataaac cacatcatca ccctggcacc tgaggacctg 720  
 gccaacctga ccgccctgcg tgtgctcgat gtgggtggga actgccgtcg ctgtgaccac 780  
 gcccgcaacc cctgtatgga gtgcccgaag ggcttccgc acctgcaccc tgacaccttc 840  
 agccacctga accacctga aggcctgggt ttgaaggaca gctctctcta caacctgaac 900

```

cccagatggt tccatgccct gggcaacctc atggtgctgg acctgagtga gaacttccta 960
tatgactgca tcacaaaaac cacagccttc cagggcctgg cccagctgcg cagactcaac 1020
ttgtctttca attaccacaa gaagggtgtcc ttgcccacc tgcattctggc gccctccttc 1080
gggagcctgc tctccctgca gcagctggac atgcatggca tcttcttcg ctcgctcagc 1140
gagaccacgc tccggctgct ggtccacctg cccatgctcc agagtctgca cctgcagatg 1200
aacttcatca atcaggccca gctcagcatc ttcggggcct tccctggcct gcgatacgtg 1260
gacctgtcag acaaccgcat aagtggagcc atggagctgg cggctgccac gggggaggtg 1320
gatggtgggg agagagtccg gctgccatct ggggacctag ctctggggcc accgggcacc 1380
cctagctccg agggcttcat gccaggctgc aagacctca acttcacctt ggacctgtca 1440
cggaacaacc tagtgacaat ccagccagag atgtttgccc ggctctcgcg cctccagtgc 1500
ctgctcctga gccgcaacag catctcgagc gcagtcaacg gtcacaatt tatgccgctg 1560
accagcctgc aggtgctgga cctgtcccat aacaagctgg acctgtacca tgggcgctct 1620
ttcacggagc tgccgcggtt ggaggccctg gacctcagct acaacagcca gcccttcagc 1680
atgcagggcg tgggtcacia cctcagcttt gtggcacagc tgccggccct gcgctatctc 1740
agcctggcgc acaacgacat ccacagccgt gtgtcccagc agctctgcag cgcctcgctg 1800
cgggccttgg acttcagcgg caatgccttg agccgatgt gggccgaggg agacctgtat 1860
ctccacttct tccgaggcct gaggagcctg gtccggttgg atctgtcca gaatcgctg 1920
cataccctct tgccacgcac cctggacaac ctccccaaga gcctgcggct gctgcgtctc 1980
cgtgacaatt atctggcttt cttcaactgg agcagcctgg tcctcctccc caggctggaa 2040
gccctggacc tggcgggaaa ccagctgaag gccctgagca acggcagctt gcctaattgga 2100
accagctcc agaggctgga cctcagcagc aacagtatca gcttcgtggc ctccagcttt 2160
tttgctctgg ccaccaggct gcgagagctc aacctcagt ccaacgccct caagacggtg 2220
gagccctcct ggttcggttc tctagcgggc accctgaaag tcctagatgt gactggcaac 2280
cccctgcact gcgcctgtgg ggcggccttc gtggacttct tgctggaggt gcaggctgca 2340
gtgcccgcc tgccaggcca cgtcaagtgt ggcagtccag gtcagctcca gggccgcagc 2400
atctttgcgc aggatctgcg cctctgcctg gatgaggccc tctcctggga ctgttttggc 2460

```

```

<210> 29
<211> 1032
<212> PRT
<213> Mus musculus

```

&lt;400&gt; 29

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn  
 50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn  
 65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met  
 100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
 130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
 145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu

225		230		235		240
Ala Asn Leu Thr Ser	Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg					
	245		250		255	
Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser						
	260		265		270	
Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly						
	275		280		285	
Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe						
	290		295		300	
Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu						
305		310		315		320
Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu						
	325		330		335	
Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala						
	340		345		350	
Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu						
	355		360		365	
Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu						
	370		375		380	
Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met						
385		390		395		400
Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala						
	405		410		415	
Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr						
	420		425		430	
Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu						
	435		440		445	
Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser						
	450		455		460	

Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu  
 465 470 475 480

Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu  
 485 490 495

Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala  
 500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp  
 515 520 525

Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu  
 530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe  
 545 550 555 560

Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser  
 565 570 575

Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val  
 580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly  
 595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe  
 610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn  
 625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu  
 645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr  
 660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn  
 675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu  
 690 695 700



Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala  
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn  
725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn  
740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly  
755 760 765

Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly  
770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg  
785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser  
805 810 815

Trp Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Met Val  
820 825 830

Val Pro Ile Leu His His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe  
835 840 845

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Ala Arg Ser Arg Arg Ser  
850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln  
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu  
885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp  
900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr  
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser  
930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His  
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
 980 985 990

Leu Phe Trp Pro Gln Gln Pro Asn Gly Gln Gly Gly Phe Trp Ala Gln  
 995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln  
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu  
 1025 1030

<210> 30  
 <211> 821  
 <212> PRT  
 <213> Mus musculus

<400> 30

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn  
 50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn  
 65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met  
 100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
 130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
 145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser  
 260 265 270

Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe  
 290 295 300

Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu  
 325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala

340	345	350
Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu		
355	360	365
Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu		
370	375	380
Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met		
385	390	395
Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala		
405	410	415
Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr		
420	425	430
Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu		
435	440	445
Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser		
450	455	460
Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu		
465	470	475
Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu		
485	490	495
Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala		
500	505	510
Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp		
515	520	525
Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu		
530	535	540
Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe		
545	550	555
Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser		
565	570	575

Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val  
 580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly  
 595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe  
 610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn  
 625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu  
 645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr  
 660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn  
 675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu  
 690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala  
 705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn  
 725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn  
 740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly  
 755 760 765

Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly  
 770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg  
 785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser  
 805 810 815

Trp Asp Cys Phe Gly  
820

<210> 31

<211> 3200

<212> DNA

<213> Mus musculus

<400> 31

```

tgtcagaggg agcctcgga gaatcctcca tctcccaaca tggttctccg tcgaaggact      60
ctgcacccct tgtccctcct ggtacaggct gcagtgtctg ctgagactct ggccctgggt      120
accctgcctg ccttcctacc ctgtgagctg aagcctcatg gcctggtgga ctgcaattgg      180
ctgttcctga agtctgtacc ccgtttctct gcggcagcat cctgctccaa catcaccgcg      240
ctctccttga tctccaaccg tatccaccac ctgcacaact ccgacttcgt ccacctgtcc      300
aacctgcggc agctgaacct caagtggaaac tgtccacca ctggccttag cccctgcac      360
ttctcttgcc acatgaccat tgagcccaga accttcctgg ctatgcgtac actggaggag      420
ctgaacctga gctataatgg tatcaccact gtgccccgac tgcccagctc cctggtgaat      480
ctgagcctga gccacaccaa catcctgggt ctagatgcta acagcctcgc cggcctatac      540
agcctgcgcg ttctcttcat ggacgggaac tgctactaca agaaccctg cacaggagcg      600
gtgaagggtga cccagggcg cctcctgggc ctgagcaatc tcaccatct gtctctgaag      660
tataacaacc tcacaaaggt gccccgcaa ctgccccca gcctggagta cctcctggtg      720
tcctataaacc tcattgtcaa gctggggcct gaagacctgg ccaatctgac ctcccttoga      780
gtacttgatg tgggtgggaa ttgccgtcgc tgcgacctg ccccaatcc ctgtatagaa      840
tgtggccaaa agtccctcca cctgcaccct gagaccttc atcacctgag ccatctggaa      900
ggcctggtgc tgaaggacag ctctctccat acactgaact cttcctgggt ccaaggctctg      960
gtcaacctct cgggtgctga cctaagcgag aactttctct atgaaagcat caaccacacc     1020
aatgcctttc agaacctaac ccgcctgcgc aagctcaacc tgtccttcaa ttaccgcaag     1080
aaggatcctt ttgcccgcct ccacctggca agttccttca agaacctggg gtcactgcag     1140
gagctgaaca tgaacggcat cttcttccgc tcgctcaaca agtacacgct cagatggctg     1200
gccgatctgc ccaaactcca cactctgcat cttcaaatga acttcatcaa ccaggcacag     1260
ctcagcatct ttggtacctt ccgagccctt cgctttgtgg acttgtcaga caatcgcatc     1320
agtgggcctt caacgctgtc agaagccacc cctgaagagg cagatgatgc agagcaggag     1380
gagctgttgt ctgcggatcc tcaccagct ccactgagca cccctgcttc taagaacttc     1440

```

atggacaggt gtaagaactt caagttcacc atggacctgt ctcggaacaa cctggtgact	1500
atcaagccag agatgtttgt caatctctca cgcctccagt gtcttagcct gagccacaac	1560
tccattgcac aggctgtcaa tggctctcag ttcttgccgc tgactaatct gcagggtgctg	1620
gacctgtccc ataacaaact ggacttgtag cactggaaat cgttcagtga gctaccacag	1680
ttgcaggccc tggacctgag ctacaacagc cagcccttta gcatgaaggg tataggccac	1740
aatttcagtt ttgtggccca tctgtccatg ctacacagcc ttagcctggc acacaatgac	1800
attcataccc gtgtgtcctc acatctcaac agcaactcag tgagggtttct tgacttcagc	1860
ggcaacggta tgggccgcat gtgggatgag gggggccttt atctccatth cttccaaggc	1920
ctgagtggcc tgctgaagct ggacctgtct caaaataacc tgcataatcct ccggccccag	1980
aaccttgaca acctcccaa gagcctgaag ctgctgagcc tccgagacaa ctacctatct	2040
ttctttaact ggaccagtct gtccttctg cccaacctgg aagtcctaga cctggcaggc	2100
aaccagctaa aggccctgac caatggcacc ctgcctaata gcacctcct ccagaaactg	2160
gatgtcagca gcaacagtat cgtctctgtg gtcccagcct tcttcgctct ggcggtcgag	2220
ctgaaagagg tcaacctcag ccacaacatt ctcaagacgg tggatcgctc ctgggttggg	2280
cccattgtga tgaacctgac agttctagac gtgagaagca accctctgca ctgtgcctgt	2340
ggggcagcct tcgtagactt actgttggag gtgcagacca aggtgcctgg cctggctaata	2400
ggtgtgaagt gtggcagccc cggccagctg caggggccgta gcatcttcgc acaggacctg	2460
cggctgtgcc tggatgaggt cctctcttgg gactgctttg gcctttcaact cttggctgtg	2520
gccgtgggca tgggtgtgcc tatactgcac catctctgcg gctgggacgt ctggtactgt	2580
tttcatctgt gcctggcatg gctacctttg ctggcccgca gccgacgcag cgcccaagct	2640
ctcccctatg atgccttcgt ggtgttcgat aaggcacaga gcgcagttgc ggactgggtg	2700
tataacgagc tgcgggtgcg gctggaggag cggcgcggtc gccgagccct acgcttgtgt	2760
ctggaggacc gagattggct gcctggccag acgctcttcg agaacctctg ggcttccatc	2820
tatgggagcc gcaagactct atttgtgctg gccacacgg accgcgtcag tggcctcctg	2880
cgcaccagct tcctgctggc tcagcagcgc ctgttggaag accgcaagga cgtggtggtg	2940
ttggtgatcc tgcgtccgga tgcccaccgc tcccgtatg tgcgactgcg ccagcgtctc	3000
tgccgccaga gtgtgctctt ctggccccag cagcccaacg ggcagggggg cttctgggccc	3060
cagctgagta cagccctgac tagggacaac cgccacttct ataaccagaa cttctgccgg	3120
ggacctacag cagaatagct cagagcaaca gctggaaaca gctgcatctt catgcctggg	3180
tcccagttg ctctgcctgc	3200

<210> 32  
 <211> 2463  
 <212> DNA  
 <213> Mus musculus

<400> 32  
 atggttctcc gtcgaaggac tctgcacccc ttgtccctcc tggtagaggc tgcagtgtctg 60  
 gctgagactc tggccctggg taccctgcct gccttcctac cctgtgagct gaagcctcat 120  
 ggccctgggtg actgcaattg gctgttcctg aagtctgtac ccggtttctc tgcggcagca 180  
 tctgtctcca acatcacccg cctctccttg atctccaacc gtatccacca cctgcacaac 240  
 tccgacttcg tccacctgtc caacctgcgg cagctgaacc tcaagtggaa ctgtccaccc 300  
 actggcctta gccccctgca cttctcttgc cacatgacca ttgagcccag aaccttcctg 360  
 gctatgcgta cactggagga gctgaacctg agctataatg gtatcaccac tgtgccccga 420  
 ctgcccagct ccctggtgaa tctgagcctg agccacacca acatcctggg tctagatgct 480  
 aacagcctcg ccggcctata cagcctgcgc gttctcttca tggacgggaa ctgctactac 540  
 aagaacccct gcacaggagc ggtgaagggtg accccaggcg ccctcctggg cctgagcaat 600  
 ctacaccatc tgtctctgaa gtataacaac ctcaaaagg tgccccgcca actgcccccc 660  
 agcctggagt acctcctggg gtctataaac ctcatgttca agctggggcc tgaagacctg 720  
 gccaatctga cctcccttcg agtacttgat gtgggtggga attgccgtcg ctgcgaccat 780  
 gcccccaatc cctgtataga atgtggccaa aagtcctcc acctgcaccc tgagaccttc 840  
 catcacctga gccatctgga aggcctgggtg ctgaaggaca gctctctcca tacactgaac 900  
 tcttcctggg tccaagggtc ggtcaacctc tcgggtgctg acctaagcga gaactttctc 960  
 tatgaaagca tcaaccacac caatgccttt cagaacctaa cccgcctgcg caagctcaac 1020  
 ctgtccttca attaccgcaa gaaggatatc tttgccgcc tccacctggc aagttccttc 1080  
 aagaacctgg tgtcactgca ggagctgaac atgaacggca tcttcttccg ctgctcaac 1140  
 aagtacacgc tcagatggct ggccgatctg cccaaactcc aactctgca tcttcaaagt 1200  
 aacttcatca accaggcaca gctcagcatc tttggtacct tccgagccct tcgctttgtg 1260  
 gacttgtcag acaatcgcat cagtgggcct tcaacgctgt cagaagccac ccctgaagag 1320  
 gcagatgatg cagagcagga ggagctgttg tctgcgatc ctcaccagc tccactgagc 1380  
 acccctgctt ctaagaactt catggacagg tgtaagaact tcaagttcac catggacctg 1440  
 tctcggaaca acctgggtgac tatcaagcca gagatgtttg tcaatctctc acgcctccag 1500  
 tgtcttagcc tgagccacaa ctccattgca caggctgtca atggctctca gttcctgcgg 1560



ctgactaatc tgcagggtgct ggacctgtcc cataacaaac tggacttgta ccaactggaaa 1620  
 tcgttcagtg agctaccaca gttgcaggcc ctggacctga gctacaacag ccagcccttt 1680  
 agcatgaagg gtataggcca caatttcagt tttgtggccc atctgtccat gctacacagc 1740  
 cttagcctgg cacacaatga cattcatacc cgtgtgtcct cacatctcaa cagcaactca 1800  
 gtgaggtttc ttgacttcag cggcaacggt atgggccgca tgtgggatga ggggggcctt 1860  
 tatctccatt tcttccaagg cctgagtggc ctgctgaagc tggacctgtc tcaaaataac 1920  
 ctgcatatcc tccggcccca gaaccttgac aacctcccca agagcctgaa gctgctgagc 1980  
 ctccgagaca actacctatc tttctttaac tggaccagtc tgccttcct gcccaacctg 2040  
 gaagtcctag acctggcagg caaccagcta aaggccctga ccaatggcac cctgcctaata 2100  
 ggcacctcc tccagaaact ggatgtcagc agcaacagta tcgtctctgt ggtcccagcc 2160  
 ttcttcgctc tggcggtcga gctgaaagag gtcaacctca gccacaacat tctcaagacg 2220  
 gtggatcgct cctggtttgg gccatttgat atgaacctga cagttctaga cgtgagaagc 2280  
 aacctctgc actgtgcctg tggggcagcc ttcgtagact tactgttgga ggtgcagacc 2340  
 aagggtgcctg gcctggctaa tgggtgtgaag tgtggcagcc ccggccagct gcagggccgt 2400  
 agcatcttcg cacaggacct ggggctgtgc ctggatgagg tcctctcttg ggactgcttt 2460  
 ggc 2463

<210> 33  
 <211> 1032  
 <212> PRT  
 <213> Homo sapiens

<400> 33

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn  
 50 55 60

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp  
 65 70 75 80

- 95 -

305					310					315					320
Tyr	Lys	Cys	Ile	Thr	Lys	Thr	Lys	Ala	Phe	Gln	Gly	Leu	Thr	Gln	Leu
				325					330					335	
Arg	Lys	Leu	Asn	Leu	Ser	Phe	Asn	Tyr	Gln	Lys	Arg	Val	Ser	Phe	Ala
			340					345					350		
His	Leu	Ser	Leu	Ala	Pro	Ser	Phe	Gly	Ser	Leu	Val	Ala	Leu	Lys	Glu
		355					360					365			
Leu	Asp	Met	His	Gly	Ile	Phe	Phe	Arg	Ser	Leu	Asp	Glu	Thr	Thr	Leu
	370					375					380				
Arg	Pro	Leu	Ala	Arg	Leu	Pro	Met	Leu	Gln	Thr	Leu	Arg	Leu	Gln	Met
385					390					395					400
Asn	Phe	Ile	Asn	Gln	Ala	Gln	Leu	Gly	Ile	Phe	Arg	Ala	Phe	Pro	Gly
			405						410					415	
Leu	Arg	Tyr	Val	Asp	Leu	Ser	Asp	Asn	Arg	Ile	Ser	Gly	Ala	Ser	Glu
			420					425					430		
Leu	Thr	Ala	Thr	Met	Gly	Glu	Ala	Asp	Gly	Gly	Glu	Lys	Val	Trp	Leu
		435					440					445			
Gln	Pro	Gly	Asp	Leu	Ala	Pro	Ala	Pro	Val	Asp	Thr	Pro	Ser	Ser	Glu
	450					455					460				
Asp	Phe	Arg	Pro	Asn	Cys	Ser	Thr	Leu	Asn	Phe	Thr	Leu	Asp	Leu	Ser
465					470					475					480
Arg	Asn	Asn	Leu	Val	Thr	Val	Gln	Pro	Glu	Met	Phe	Ala	Gln	Leu	Ser
				485					490					495	
His	Leu	Gln	Cys	Leu	Arg	Leu	Ser	His	Asn	Cys	Ile	Ser	Gln	Ala	Val
			500					505					510		
Asn	Gly	Ser	Gln	Phe	Leu	Pro	Leu	Thr	Gly	Leu	Gln	Val	Leu	Asp	Leu
		515					520					525			
Ser	Arg	Asn	Lys	Leu	Asp	Leu	Tyr	His	Glu	His	Ser	Phe	Thr	Glu	Leu
530						535					540				

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Gly  
 545 550 555 560

Met Gln Gly Val Gly His Asn Phe Ser Phe Val Ala His Leu Arg Thr  
 565 570 575

Leu Arg His Leu Ser Leu Ala His Asn Asn Ile His Ser Gln Val Ser  
 580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn  
 595 600 605

Ala Leu Gly His Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe  
 610 615 620

Gln Gly Leu Ser Gly Leu Ile Trp Leu Asp Leu Ser Gln Asn Arg Leu  
 625 630 635 640

His Thr Leu Leu Pro Gln Thr Leu Arg Asn Leu Pro Lys Ser Leu Gln  
 645 650 655

Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser  
 660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg  
 675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg  
 690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe  
 705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
 725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu  
 740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
 755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu  
 770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser  
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp  
805 810 815

Asp Cys Phe Ala Leu Ser Leu Leu Ala Val Ala Leu Gly Leu Gly Val  
820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His  
835 840 845

Leu Cys Leu Ala Trp Leu Pro Trp Arg Gly Arg Gln Ser Gly Arg Asp  
850 855 860

Glu Asp Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Thr Gln  
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Gly Gln Leu Glu  
885 890 895

Glu Cys Arg Gly Arg Trp Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp  
900 905 910

Trp Leu Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr  
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser  
930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Gly Arg  
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln  
995 1000 1005

Leu Gly Met Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg  
1010 1015 1020

Asn Phe Cys Gln Gly Pro Thr Ala Glu  
1025 1030

<210> 34  
<211> 820  
<212> PRT  
<213> Homo sapiens  
  
<400> 34

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln  
1 5 10 15

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe  
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn  
50 55 60

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp  
65 70 75 80

Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp  
85 90 95

Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met  
100 105 110

Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
115 120 125

Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser  
130 135 140

Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser  
145 150 155 160

Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly  
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro  
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe  
 260 265 270

Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe  
 290 295 300

Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu  
 325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala  
 340 345 350

His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu  
 370 375 380

Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu

420	425	430
Leu Thr Ala Thr Met Gly Glu Ala Asp Gly Gly Glu Lys Val Trp Leu		
435	440	445
Gln Pro Gly Asp Leu Ala Pro Ala Pro Val Asp Thr Pro Ser Ser Glu		
450	455	460
Asp Phe Arg Pro Asn Cys Ser Thr Leu Asn Phe Thr Leu Asp Leu Ser		
465	470	475
480		
Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser		
485	490	495
His Leu Gln Cys Leu Arg Leu Ser His Asn Cys Ile Ser Gln Ala Val		
500	505	510
Asn Gly Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu		
515	520	525
Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu		
530	535	540
Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Gly		
545	550	555
560		
Met Gln Gly Val Gly His Asn Phe Ser Phe Val Ala His Leu Arg Thr		
565	570	575
Leu Arg His Leu Ser Leu Ala His Asn Asn Ile His Ser Gln Val Ser		
580	585	590
Gln Gln Leu Cys Ser Thr Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn		
595	600	605
Ala Leu Gly His Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe		
610	615	620
Gln Gly Leu Ser Gly Leu Ile Trp Leu Asp Leu Ser Gln Asn Arg Leu		
625	630	635
640		
His Thr Leu Leu Pro Gln Thr Leu Arg Asn Leu Pro Lys Ser Leu Gln		
645	650	655



Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser  
660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg  
675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg  
690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe  
705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu  
740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu  
770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser  
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp  
805 810 815

Asp Cys Phe Ala  
820

<210> 35

<211> 3352

<212> DNA

<213> Homo sapiens

<400> 35

aggctggtat aaaaatctta cttcctctat tctctgagcc gctgctgccc ctgtgggaag 60

ggacctcgag tgtgaagcat ccttccctgt agctgctgtc cagtctgccc gccagacctt 120

ctggagaagc ccttgccccc cagcatgggt ttctgccgca gcgccctgca cccgctgtct 180

ctcctgggtgc aggccatcat gctggccatg accctggccc tgggtacctt gcctgccttc 240

ctaccctgtg agctccagcc ccacggcctg gtgaactgca actggctgtt cctgaagtct 300

```

gtgccccact tctccatggc agcacccccgt ggcaatgtca ccagcctttc cttgtcctcc 360
aaccgcatcc accacctcca tgattctgac tttgccacc tgccagcct gcggcatctc 420
aacctcaagt ggaactgccc gccggttgcc ctgagcccca tgcacttccc ctgccacatg 480
accatcgagc ccagcacctt cttggctgtg cccaccctgg aagagctaaa cctgagctac 540
aacaacatca tgactgtgcc tgcgctgccc aaatccctca tatccctgtc cctcagccat 600
accaacatcc tgatgctaga ctctgccagc ctgcccggcc tgcattgccct gcgcttccta 660
ttcatggacg gcaactgtta ttacaagaac ccctgcaggc aggcactgga ggtggccccc 720
ggtgccctcc ttggcctggg caacctcacc cacctgtcac tcaagtacaa caacctcact 780
gtggtgcccc gcaacctgcc ttccagcctg gagtatctgc tgttgtccta caaccgcatc 840
gtcaaaactgg cgctgagga cctggccaat ctgaccgccc tgcgtgtgct cgatgtgggc 900
ggaaattgcc gccgctgcca ccacgctccc aaccctgca tggagtgcc tgcacttc 960
ccccagctac atcccagatc cttcagccac ctgagccgtc ttgaaggcct ggtgttgaag 1020
gacagttctc tctcctggct gaatgccagt tggttccgtg ggctgggaaa cctccgagt 1080
ctggacctga gtgagaactt cctctacaaa tgcattacta aaaccaaggc cttccagggc 1140
ctaacacagc tgcgcaagct taacctgtcc ttcaattacc aaaagagggt gtcctttgcc 1200
cacctgtctc tggccccttc cttcgggagc ctggtcgccc tgaaggagct ggacatgcac 1260
ggcatcttct tccgctcact cgatgagacc acgctccggc cactggcccg cctgcccatg 1320
ctccagactc tgcgtctgca gatgaacttc atcaaccagg cccagctcgg catcttcagg 1380
gccttccctg gcctgcgcta cgtggacctg tcggacaacc gcatcagcgg agcttcggag 1440
ctgacagcca ccatggggga ggcagatgga ggggagaagg tctggctgca gcctggggac 1500
cttgctccgg cccagtgga cactcccagc tctgaagact tcaggcccaa ctgcagcacc 1560
ctcaacttca ccttgatct gtcacggaac aacctggtga ccgtgcagcc ggagatgttt 1620
gcccagctct cgcacctgca gtgcctgcgc ctgagccaca actgcatctc gcaggcagtc 1680
aatggctccc agttcctgcc gctgaccggc ctgcagggtc tagacctgtc ccgcaataag 1740
ctggacctct accacgagca ctcatcagc gagctaccgc gactggaggc cctggacctc 1800
agctacaaca gccagccctt tggcatgcag ggcgtgggccc acaacttcag cttcgtggct 1860
cacctgcgca ccctgcgcca cctcagcctg gccacaaca acatccacag ccaagtgtcc 1920
cagcagctct gcagtacgtc gctgcgggccc ctggacttca gcggcaatgc actgggccc 1980
atgtgggccc agggagacct ctatctgcac ttcttccaag gcctgagcgg ttgatctgg 2040

```

ctggacttgt cccagaaccg cctgcacacc ctctgcccc aaacctgcg caacctcccc 2100  
 aagagcctac aggtgctgcg tctccgtgac aattacctgg ccttctttaa gtggtggagc 2160  
 ctccacttcc tgcccaaact ggaagtcctc gacctggcag gaaaccggct gaaggccctg 2220  
 accaatggca gcctgcctgc tggcaccgag ctccggaggc tggatgtcag ctgcaacagc 2280  
 atcagcttgc tggcccccg cttcttttcc aaggccaagg agctgcgaga gctcaacctt 2340  
 agcgccaacg ccctcaagac agtggaccac tcctggtttg ggccctggc gaggccctg 2400  
 caaatactag atgtaagcgc caacctctg cactgcgcct gtggggcggc ctttatggac 2460  
 ttctgctgg aggtgcagc tgcctgccc ggtctgcca gccgggtgaa gtgtggcagt 2520  
 ccgggccagc tccagggcct cagcatcttt gcacaggacc tgcgcctctg cctggatgag 2580  
 gccctctct gggactgttt cgcctctctg ctgctggctg tggctctggg cctgggtgtg 2640  
 cccatgctgc atcacctctg tggctgggac ctctggtact gcttccacct gtgcctggcc 2700  
 tggcttccct ggccggggcg gcaaagtgg cgagatgagg atgccctgcc ctacgatgcc 2760  
 ttctggtct tcgacaaaac gcagagcgca gtggcagact ggggtgtaca cgagcttcgg 2820  
 gggcagctgg aggagtgcg tgggcgctgg gcaactcgcc tgtgcctgga ggaacgcgac 2880  
 tggctgcctg gcaaaacct ctttgagaac ctgtgggcct cggctctatg cagccgcaag 2940  
 acgctgtttg tgctggcca caccgaccgg gtcagtggc tcttgccgc cagcttctg 3000  
 ctggcccagc agcgctgct ggaggaccgc aaggacgtc tgggtgctgg gatcctgagc 3060  
 cctgacggcc gccgctccc ctacgtgcgg ctgcgccagc gcctctgcc ccagagtgtc 3120  
 ctctctggc cccaccagc cagtggtcag cgcagcttct gggcccagct gggcatggc 3180  
 ctgaccagg acaaccacca cttctataac cggaaactt gccagggacc caccggcgaa 3240  
 tagccgtgag ccggaatcct gcacggtgcc acctccacac tcacctcacc tctgcctgcc 3300  
 tggctctgacc ctccctgct cgcctccctc accccacacc tgacacagag ca 3352

&lt;210&gt; 36

&lt;211&gt; 2460

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 36

atgggtttct gccgcagcgc cctgcacccg ctgtctctcc tgggtcaggc catcatgctg 60  
 gccatgaccc tggccctggg taccttgccct gccttcctac cctgtgagct ccagccccac 120  
 ggctggtga actgcaactg gctgttctct aagtctgtgc ccacttctc catggcagca 180  
 cccgctggca atgtcaccag cctttccttg tcctccaacc gcatccacca cctccatgat 240

tctgactttg cccacctgcc cagcctgcgg catctcaacc tcaagtggaa ctgcccgcg	300
gttggcctca gcccacatgca cttcccctgc cacatgacca tcgagcccag caccttcttg	360
gctgtgcca ccttgaaga gctaaacctg agctacaaca acatcatgac tgtgcctgcg	420
ctgcccacaaat ccctcatatc cctgtccctc agccatacca acatcctgat gctagactct	480
gccagcctcg cgggcctgca tgccctgcgc ttcctattca tggacggcaa ctgttattac	540
aagaacccct gcaggcaggc actggagggtg gccccgggtg ccctccttgg cctgggcaac	600
ctcaccacacc tgtcactcaa gtacaacaac ctactgttg tgccccgcaa cctgccttcc	660
agcctggagt atctgctgtt gtccataaac cgcctcgtca aactggcgcc tgaggacctg	720
gccaatctga cggccctgcg tgtgctcgat gtgggaggaa attgccgcg ctgcgaccac	780
gtcccaacc cctgcatgga gtgcctcgt cacttcccc agctacatcc cgataccttc	840
agccacctga gccgtcttga aggcctggtg ttgaaggaca gttctctctc ctggctgaat	900
gccagttggt tccgtgggct gggaaacctc cgagtgttg acctgagtga gaacttctc	960
tacaaatgca tcactaaaac caaggccttc cagggcctaa cacagctgcg caagcttaac	1020
ctgtccttca attacaaaa gaggggtgtcc ttgcccacc tgtctctggc cccttcttc	1080
gggagcctgg tcgccctgaa ggagctggac atgcacggca tcttcttccg ctactcgat	1140
gagaccacgc tccggccact ggcccgctg cccatgctcc agactctgcg tctgcagatg	1200
aacttcatca accaggccca gctcggcatc ttcaggcct tccctggcct gcgtacgtg	1260
gacctgtcgg acaaccgcat cagcggagct tcggagctga cagccaccat gggggaggca	1320
gatggagggg agaaggctctg gctgcagcct ggggaccttg ctccggcccc agtggacact	1380
cccagctctg aagacttcag gcccactgc agcaccctca acttcacctt ggatctgtca	1440
cggaaacaacc tgggtgaccgt gcagcggag atgtttgcc agctctcgca cctgcagtgc	1500
ctgcgcctga gccacaactg catctcgcag gcagtcaatg gctcccagtt cctgccgctg	1560
accggctctg aggtgctaga cctgtccgc aataagctgg acctctacca cgagcactca	1620
ttcacggagc taccgcgact ggaggccctg gacctcagct acaacagcca gccctttggc	1680
atgcagggcg tgggccacaa cttcagcttc gtggctcacc tgcgaccct gcgccacctc	1740
agcctggccc acaacaacat ccacagccaa gtgtcccagc agctctgcag tacgtcgtg	1800
cgggcccctg acttcagcgg caatgcactg ggccatatgt gggccgagg agacctctat	1860
ctgcacttct tccaaggcct gagcggtttg atctggctgg acttgtccca gaaccgctg	1920
cacaccctcc tgccccaaac cctgcgcaac ctccccaaaga gcctacaggt gctgcgtctc	1980
cgtgacaatt acctggcctt ctttaagtgg tggagcctcc acttctgcc caaactggaa	2040

gtcctcgacc tggcaggaaa cgggctgaag gccctgacca atggcagcct gcctgctggc 2100  
 acccggtctc ggaggctgga tgtcagctgc aacagcatca gcttcgtggc ccccggttc 2160  
 ttttccaagg ccaaggagct gcgagagctc aaccttagcg ccaacgccct caagacagtg 2220  
 gaccactcct ggtttggggc cctggcgagt gccctgcaaa tactagatgt aagcgccaac 2280  
 cctctgcact gcgcctgtgg ggcgcccttt atggacttcc tgctggaggt gcaggctgcc 2340  
 gtgcccggtc tgcccagccg ggtgaagtgt ggcagtccgg gccagctcca gggcctcagc 2400  
 atctttgcac aggacctgcg cctctgcctg gatgaggccc tctcctggga ctgtttcgcc 2460

<210> 37

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 37

accttgctg ccttcctacc ctgtga

26

<210> 38

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 38

gtccgtgtgg gccagcaca a

21

<210> 39

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 39

tccatgacgt ttttgatgtt

20

<210> 40

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 40  
tccataacgt ttttgatggt 20

<210> 41  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 41  
tccatcacgt ttttgatggt 20

<210> 42  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 42  
tccattacgt ttttgatggt 20

<210> 43  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 43  
tccatggcgt ttttgatggt 20

<210> 44  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 44  
tccatgccgt ttttgatggt 20

<210> 45  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 45

tccatgtcgt ttttgatggt

20

<210> 46

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 46

tccatgatgt ttttgatggt

20

<210> 47

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 47

tccatgaagt ttttgatggt

20

<210> 48

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 48

tccatgaggt ttttgatggt

20

<210> 49

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 49

tccatgacat ttttgatggt

20

<210> 50

<211> 20

<212> DNA

<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 50  
tccatgacct ttttgatggt 20

<210> 51  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 51  
tccatgactt ttttgatggt 20

<210> 52  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 52  
tccatgacgc ttttgatggt 20

<210> 53  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 53  
tccatgacga ttttgatggt 20

<210> 54  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 54  
tccatgacgg ttttgatggt 20

<210> 55  
<211> 20  
<212> DNA  
<213> Artificial sequence



<220>  
<223> Synthetic oligonucleotide

<400> 55  
tccatgacgt ctttgatggt 20

<210> 56  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 56  
tccatgacgt atttgatggt 20

<210> 57  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 57  
tccatgacgt gtttgatggt 20

<210> 58  
<211> 24  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 58  
tcgctgctttt gtcgcttttgt cggt 24

<210> 59  
<211> 24  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 59  
tgctgctttt gtgcttttgt gctt 24

<210> 60  
<211> 20  
<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 60

tccatgacgt tcctgatgct

20

<210> 61

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 61

tccatgagct tcctgatgct

20

<210> 62

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> Consensus oligopeptide

<220>

<221> MISC\_FEATURE

<222> (4)..(5)

<223> Any amino acid

<220>

<221> MISC\_FEATURE

<222> (7)..(12)

<223> Any amino acid

<220>

<221> MISC\_FEATURE

<222> (14)..(15)

<223> Any amino acid

<400> 62

Gly Asn Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys  
1 5 10 15

<210> 63

<211> 16

<212> PRT

<213> Homo sapiens

<400> 63

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys  
 1 5 10 15

<210> 64  
 <211> 16  
 <212> PRT  
 <213> Mus musculus

<400> 64

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Ile Cys  
 1 5 10 15

<210> 65  
 <211> 31  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Consensus oligopeptide

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(8)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (10)..(10)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (12)..(12)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(22)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (25)..(30)  
 <223> Any amino acid

<400> 65

Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Asp Xaa Tyr Xaa Xaa Xaa  
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Ser Xaa Xaa Xaa Xaa Xaa Xaa Tyr  
                   20                                  25                                  30

<210> 66  
 <211> 31  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(8)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (10)..(10)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (12)..(12)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(22)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (25)..(30)  
 <223> Any amino acid

<400> 66

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa  
 1                                  5                                  10                                  15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Tyr  
                   20                                  25                                  30

<210> 67  
 <211> 31  
 <212> PRT  
 <213> Mus musculus

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(8)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (10)..(10)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (12)..(12)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(22)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (25)..(30)  
 <223> Any amino acid

<400> 67

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa  
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Gln Leu Xaa Xaa Xaa Xaa Xaa Tyr  
 20 25 30

<210> 68  
 <211> 31  
 <212> PRT  
 <213> Homo sapiens

<400> 68

Gln Val Leu Asp Leu Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His  
 1 5 10 15

Ser Phe Thr Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr  
 20 25 30

<210> 69  
 <211> 31  
 <212> PRT  
 <213> Mus musculus

<400> 69

Gln Val Leu Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys

```
<210> 70
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 70
tccaggactt ctctcaggtt
```